

11-88L.ST25.txt
SEQUENCE LISTING

<110> Seed, Brian
Aruffo, Alejandro
Camerini, David

<120> CD27 Coding Sequence

<130> 11-88L

<140> US 09/836,544
<141> 2001-04-17

<150> US 07/983,647
<151> 1992-12-01

<150> US 07/553,759
<151> 1990-07-13

<150> US 07/498,809
<151> 1990-03-23

<150> US 07/379,076
<151> 1989-07-13

<150> US 07/160,416
<151> 1988-02-25

<160> 41

<170> PatentIn version 3.3

<210> 1
<211> 2932
<212> DNA
<213> artificial

<220>
<223> Nucleotide sequence of pIH3 vector

<400> 1
ggcgtaatct gctgcttgca aacaaaaaaa ccaccgctac cagcgggtgt tgttttgccg 60
gatcaagagc taccaactct ttttccgaag gaactggctt cagcagagcg cagataccaa 120
atactgtcct tctagtgtag ccgtagttag gccaccactt caagaactct gttagcaccgc 180
ctacatacct cgtctgtcta atcctgttac cagtggctgc tgccagtggc gataagtcgt 240
gtcttaccgg gttggactca agacgatagt taccggataa ggcgcagcgg tcgggctgaa 300
cgggggggtt cgtgcacacag ccagccttgg agcgaacgac ctacaccgaa ctgagatacc 360
tacagcgtga gctatgagaa agcgccacgc ttcccgaagg gagaaggcgg gacaggtatc 420
cggtaaaggc cagggtcgga acaggagagc gcacgagggg gcttccaggg ggaacgcct 480
ggtatcttta tagtctgtc gggtttcgcc acctctgact tgagcgtcga tttttgtgat 540
gctcgtcagg ggggcggagc ctatggaaaa acgccagcaa cgccgaatta ccgcggtgtt 600
tctcaacgta acatttaca gcggcgcgtc atttgatatg atgcgccccg cttcccgata 660

agggagcagg ccagtaaaag cattaccctg ggtgggggtc ccgagcggcc aaaggagca	720
gactctaaat ctgccgtcat cgacttcgaa ggttcgaatc ctccccccac caccatcaact	780
ttcaaaagtc cgaagaatc tgctccctgc ttgtgtgttg gaggtcgctg agtagtgccg	840
gagtaaaatt taagctacaa caaggcaagg cttgaccgac aattgcataga agaattcgct	900
taggggttagg cgttttcgcg tgcttcgca tgtacgggcc agatatacgc gttgacattg	960
attattgact agttattaat agtaataat tacgggggtca ttagttcata gcccatatat	1020
ggagttccgc gttacataac ttacggtaaa tggcccgctt ggctgaccgc ccaacgaccc	1080
ccgcccattg acgtcaataa tgacgtatgt tcccatagta acgccaatag ggactttcca	1140
ttgacgtcaa tgggtggact atttacggta aactgcccac ttggcagtac atcaagtgt	1200
tcatacgcca agtacgcccc ctattgacgt caatgacggt aaatggcccg cctggcatta	1260
tgcccagtac atgaccttat gggactttcc tacttggcag tacatctacg tattagtcac	1320
cgctattacc atgggtgatgc ggttttgcca gtacatcaat gggcgtagg agcggttga	1380
ctcacgggga ttcccaagtc tccaccccat tgacgtcaat gggagtttgt ttggcacca	1440
aaatcaacgg gactttccaa aatgtcgtaa caactccgcc ccattgacgc aaatggcg	1500
aattcctggg cgggactggg gaggggcgag ccctcagatg ctgcatataa gcagctgctt	1560
tttgctgta ctgggtctct ctgggttagac cagatctgag cctgggagct ctctggctaa	1620
ctagagaacc cactgcttaa gcctcaataa agctcttaga gatccctcga cctcgaggga	1680
tcttccatac ctaccagttc tgcgcctgca ggtcgcgccc gcgactctag aggatctttg	1740
tgaaggaacc ttacttctgt ggtgtgacat aattggacaa actacctaca gagatttaaa	1800
gctctaagggt aaatataaaa tttttaagtg tataatgtgt taaactactg attctaattg	1860
tttgtgtatt ttgattcca acctatggaa ctgatgaatg ggagcagtg tggaatgcct	1920
ttaatgagga aaacctgttt tgctcagaag aaatgccatc tagtgatgat gaggctactg	1980
ctgactctca acattctact cctccaaaaa agaagagaaa ggtagaagac cccaaggact	2040
ttccttcaga attgctaagt tttttgagtc atgctgtgtt tagtaataga actcttgctt	2100
gctttgctat ttacaccaca aaggaaaaag ctgcactgct atacaagaaa attatggaaa	2160
aatattctgt aacctttata agtaggcata acagttataa tcataacata ctgttttttc	2220
ttactccaca caggcataga gtgtctgcta ttaataacta tgctcaaaaa ttgtgtacct	2280
ttagcttttt aatttgtaaa ggggttaata aggaatattt gatgtatagt gccttgacta	2340
gagatcataa tcagccatac cacatttgta gaggttttac ttgctttaaa aaacctcca	2400
cacctcccc tgaacctgaa acataaaatg aatgcaattg ttgtgttaa cttgtttatt	2460
gcagcttata atggttacaa ataaagcaat agcatcacia atttcacaaa taaagcattt	2520
ttttcactgc attctagtgt tgggttgctc aaactcatca atgtatctta tcatgtctgg	2580

11-88L.ST25.txt

```

atcctgtgga atgtgtgtca gttaggggtgt ggaaagtccc caggctcccc agcaggcaga 2640
agtatgcaaa gcatgcatct caattagtca gcaaccagggt gtggaaagtc cccaggctcc 2700
ccagcaggca gaagtatgca aagcatgcat ctcaattagt cagcaacccat agtccccgcc 2760
ctaactccgc ccatcccgcc cctaactccg cccagttccg cccattctcc gccccatggc 2820
tgactaatTT tttttatTTa tgcagaggcc gaggcgcct cggcctctga gctattccag 2880
aagtagtgag gaggcttttt tggaggccta ggctttttga aaaagctaat tc 2932

```

```

<210> 2
<211> 1504
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (7)..(1059)

```

```

<400> 2
cctaag atg agc ttt cca tgt aaa ttt gta gcc agc ttc ctt ctg att 48
Met Ser Phe Pro Cys Lys Phe Val Ala Ser Phe Leu Leu Ile
1 5 10

ttc aat gtt tct tcc aaa ggt gca gtc tcc aaa gag att acg aat gcc 96
Phe Asn Val Ser Ser Lys Gly Ala Val Ser Lys Glu Ile Thr Asn Ala
15 20 25 30

ttg gaa acc tgg ggt gcc ttg ggt cag gac atc aac ttg gac att cct 144
Leu Glu Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro
35 40 45

agt ttt caa atg agt gat gat att gac gat ata aaa tgg gaa aaa act 192
Ser Phe Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr
50 55 60

tca gac aag aaa aag att gca caa ttc aga aaa gag aaa gag act ttc 240
Ser Asp Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe
65 70 75

aag gaa aaa gat aca tat aag cta ttt aaa aat gga act ctg aaa att 288
Lys Glu Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile
80 85 90

aag cat ctg aag acc gat gat cag gat atc tac aag gta tca ata tat 336
Lys His Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr
95 100 105 110

gat aca aaa gga aaa aat gtg ttg gaa aaa ata ttt gat ttg aag att 384
Asp Thr Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile
115 120 125

caa gag agg gtc tca aaa cca aag atc tcc tgg act tgt atc aac aca 432
Gln Glu Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr
130 135 140

acc ctg acc tgt gag gta atg aat gga act gac ccc gaa tta aac ctg 480
Thr Leu Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu
145 150

```

11-88L.ST25.txt

145	150	155	
tat caa gat ggg aaa cat cta aaa ctt tct cag agg gtc atc aca cac			528
Tyr Gln Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His			
160	165	170	
aag tgg acc acc agc ctg agt gca aaa ttc aag tgc aca gca ggg aac			576
Lys Trp Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn			
175	180	185	190
aaa gtc agc aag gaa tcc agt gtc gag cct gtc agc tgt cca gag aaa			624
Lys Val Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys			
195	200	205	
ggg ctg gac atc tat ctc atc att ggc ata tgt gga gga ggc agc ctc			672
Gly Leu Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Ser Leu			
210	215	220	
ttg atg gtc ttt gtg gca ctg ctc gtt ttc tat atc acc aaa agg aaa			720
Leu Met Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys			
225	230	235	
aaa cag agg agt cgg aga aat gat gag gag ctg gag aca aga gcc cac			768
Lys Gln Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His			
240	245	250	
aga gta gct act gaa gaa agg ggc cgg aag ccc cac caa att cca gct			816
Arg Val Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala			
255	260	265	270
tca acc cct cag aat cca gca act tcc caa cat cct cct cca cca cct			864
Ser Thr Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Pro			
275	280	285	
ggg cat cgt tcc cag gca cct agt cat cgt ccc cgg cct cct gga cac			912
Gly His Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Gly His			
290	295	300	
cgt gtt cag cac cag cct cag aag agg cct cct gct ccg tgg ggc aca			960
Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr			
305	310	315	
caa gtt cac cag cag aaa ggc ccg ccc ctc ccc aga cct cga gtt cag			1008
Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln			
320	325	330	
cca aaa cct ccc cat ggg gca gca gaa aac tca ttg tcc cct tcc tct			1056
Pro Lys Pro Pro His Gly Ala Ala Glu Asn Ser Leu Ser Ser Ser Ser			
335	340	345	350
aat taaaaaagat agaaaactgtc tttttcaata aaaagcactg tggatttctg			1109
Asn			
ccctcctgat gtgcatatcc gtacttccat gaggtgtttt ctgtgtgcag aacattgtca			1169
cctcctgagg ctgtgggccca cagccacctc tgcattctcg aactcagcca tgtggccaac			1229
atctggagtt tttgtcttc tcagagagct ccatcacacc agtaaggaga agcaatataa			1289
gtgtgattgc aagaatggta gaggaccgag cacagaaatc ttagagattt cttgtcccct			1349
ctcagggtcat gtgtagatgc gataaatcaa gtgattgggtg tgcctggggtc tcaactacaag			1409

11-88L.ST25.txt

cagcctatct gcttaagaga ctctggagtt tcttatgtgc cctggaggac acttgccac 1469
 catcctgtga gtaaaagtga aataaaagct ttgac 1504

<210> 3
 <211> 351
 <212> PRT
 <213> Homo sapiens

<400> 3

Met Ser Phe Pro Cys Lys Phe Val Ala Ser Phe Leu Leu Ile Phe Asn
 1 5 10 15
 Val Ser Ser Lys Gly Ala Val Ser Lys Glu Ile Thr Asn Ala Leu Glu
 20 25 30
 Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro Ser Phe
 35 40 45
 Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr Ser Asp
 50 55 60
 Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe Lys Glu
 65 70 75 80
 Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile Lys His
 85 90 95
 Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr Asp Thr
 100 105 110
 Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile Gln Glu
 115 120 125
 Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr Thr Leu
 130 135 140
 Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln
 145 150 155 160
 Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp
 165 170 175
 Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn Lys Val
 180 185 190
 Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu
 195 200 205

11-88L.5T25.txt

Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu Leu Met
 210 215 220

Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys Lys Gln
 225 230 235 240

Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His Arg Val
 245 250 255

Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala Ser Thr
 260 265 270

Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Pro Gly His
 275 280 285

Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His Arg Val
 290 295 300

Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr Gln Val
 305 310 315 320

His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln Pro Lys
 325 330 335

Pro Pro His Gly Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser Asn
 340 345 350

<210> 4
 <211> 874
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (13)..(723)

<400> 4
 gcccgacgag cc atg gtt gct ggg agc gac gcg ggg cgg gcc ctg ggg gtc 51
 Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val
 1 5 10

ctc agc gtg gtc tgc ctg ctg cac tgc ttt ggt ttc atc agc tgt ttt 99
 Leu Ser Val Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe
 15 20 25

tcc caa caa ata tat ggt gtt gtg tat ggg aat gta act ttc cat gta 147
 Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val
 30 35 40 45

cca agc aat gtg cct tta aaa gag gtc cta tgg aaa aaa caa aag gat 195
 Pro Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp
 Page 6

11-88L.ST25.txt

50										55										60										
aaa gtt gca gaa ctg gaa aat tct gaa ttc aga gct ttc tca tct ttt	243																													
Lys Val Ala Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Phe																														
65	70	75																												
aaa aat agg gtt tat tta gac act gtg tca ggt agc ctc act atc tac	291																													
Lys Asn Arg Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr																														
80	85	90																												
aac tta aca tca tca gat gaa gat gag tat gaa atg gaa tcg cca aat	339																													
Asn Leu Thr Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn																														
95	100	105																												
att act gat acc atg aag ttc ttt ctt tat gtg ctt gag tct ctt cca	387																													
Ile Thr Asp Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro																														
110	115	120	125																											
tct ccc aca cta act tgt gca ttg act aat gga agc att gaa gtc caa	435																													
Ser Pro Thr Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln																														
130	135	140																												
tgc atg ata cca gag cat tac aac agc cat cga gga ctt ata atg tac	483																													
Cys Met Ile Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr																														
145	150	155																												
tca tgg gat tgt cct atg gag caa tgt aaa cgt aac tca acc agt ata	531																													
Ser Trp Asp Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile																														
160	165	170																												
tat ttt aag atg gaa aat gat ctt cca caa aaa ata cag tgt act ctt	579																													
Tyr Phe Lys Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu																														
175	180	185																												
agc aat cca tta ttt aat aca aca tca tca atc att ttg aca acc tgt	627																													
Ser Asn Pro Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys																														
190	195	200	205																											
atc cca agc agc ggt cat tca aga cac aga tat gca ctt ata ccc ata	675																													
Ile Pro Ser Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile																														
210	215	220																												
cca tta gca gta att aca aca tgt att gtg ctg tat atg aat gtt ctt	723																													
Pro Leu Ala Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Val Leu																														
225	230	235																												
taattgagaa gacaattttt tcatttttag gtattctgaa atgtgacaga aaaccagaca	783																													
gaaccaactc caattgattg gtaacagaag atgaagacaa cagcataact aaattatttt	843																													
aaaaactaaa aagccatctg atttctcatt t	874																													
<210> 5																														
<211> 237																														
<212> PRT																														
<213> Homo sapiens																														
<400> 5																														
Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val																														
1 5 10 15																														

11-88L.ST25.txt

Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
20 25 30

Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
35 40 45

Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
50 55 60

Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
65 70 75 80

Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
85 90 95

Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
100 105 110

Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
115 120 125

Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
130 135 140

Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
145 150 155 160

Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys
165 170 175

Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
180 185 190

Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
195 200 205

Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala
210 215 220

Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Val Leu
225 230 235

<210> 6
<211> 3900
<212> DNA
<213> Artificial
<220>

11-88L.ST25.txt

<223> Nucleotide sequence of the pIH3M vector.

```

<400> 6
ggcgtaatct gctgcttgca aacaaaaaaaa ccaccgctac cagcggtggt ttgtttgccg      60
gatcaagagc taccaactct ttttccgaag gtaactggct tcagcagagc gcagatacca      120
aatactgtcc ttctagtgtg gccgtagtta ggccaccact tcaagaactc tgtagcaccg      180
cctacatacc tcgctctgct aatcctgtta ccagtggctg ctgccagtgg cgataagtcg      240
tgtcttaccg ggttggactc aagacgatag ttaccggata aggcgcagcg gtcgggctga      300
acgggggggt cgtgcacaca gcccgacttg gagcgaacga cctacaccga actgagatac      360
ctacagcgtg agcattgaga aagcgccacg cttcccgaag ggagaaagcg gacaggtat      420
ccggtaaagc gcaggggtcg aacaggagag cgcacgaggg agcttccagg ggaacgcgc      480
tggtatcttt atagtctgtg cgggtttcgc cactctgac ttgagcgtcg atttttgtga      540
tgctcgtcag gggggcgagg cctatggaaa aacgccagca acgcaagcta gcttctagct      600
agaaattgta aacgttaata ttttgttaaa attcgcgtta aatttttgtt aaatcagctc      660
attttttaac caataggccg aaatcggcaa aatcccttat aaatcaaaag aatagcccga      720
gatagggttg agtggtgttc cagtttgtaa caagagtcca ctattaaaga acgtggactc      780
caacgtcaaa gggcgaaaaa ccgtctatca gggcgatggc cgccactac gtgaaccatc      840
acccaatatc agttttttgg ggtcgagggt ccgtaaagca ctaaatcgga accctaaagg      900
gagccccgga tttagagctt gacggggaaa gccggcgaac gtggcgagaa aggaagggaa      960
gaaagcgaaa ggagcgggct ctagggcgct ggcaagtgtg gcggtcacgc tgcgcgtaac     1020
caccacaccc gccgcgctta atgcgccgct acagggcgcg tactatggtt gctttgacga     1080
gcacgtataa cgtgcttttc tcgttggaat cagagcggga gctaaacagg aggccgatta     1140
aagggatttt agacaggaac ggtacgccag ctggatcacc gcggtctttc tcaacgtaac     1200
actttacagc ggcgcgtcat ttgatatgat gcgccccgct tcccgataag ggagcaggcc     1260
agtaaaagca ttaccctggt tggggttccc gagcggccaa agggagcaga ctctaaatct     1320
gccgtcatcg acttcgaagg ttcaatcct tccccacca ccatcacttt caaaagtccg     1380
aaagaatctg ctccctgctt gtgtgttgga ggtcgttgag tagtcgcgga gtaaaattta     1440
agctacaaca aggcaaggct tgaccgacaa ttgcatgaag aatctgctta gggttaggcg     1500
ttttgcgctg cttcgcgatg tacgggccag atatacgcgt tgacattgat tattgactag     1560
ttattaatag taatcaatta cggggtcatt agttcatagc ccatatatgg agttccgcgt     1620
tacataaact acggtaaatg gcccgcctgg ctgaccgcc aacgaccccc gccattgac     1680
gtcaataatg acgtatgttc ccatagtaac gccaataggg actttccatt gacgtcaatg     1740
ggtggactat ttacggtaaa ctgccactt ggcagtcacat caagtgtatc atatgccaag     1800

```

tacgccccct attgacgtca atgacggtaa atggcccgcc tggcattatg cccagttacat	1860
gaccttatgg gacttttcta cttggcagta catctacgta ttagtcatcg ctattaccat	1920
gggtgatgcg ttttggcagt acatcaatgg gcgtggatag cggtttgact cacggggatt	1980
tccaagtctc caccctattg acgtcaatgg gagtttgttt tggcaccaaa atcaacggga	2040
ctttccaaaa tgtcgtaaca actccgcccc attgacgcaa atggcgaggaa ttcctgggcg	2100
ggactgggga gtggcgagcc ctgagatgct gcatataagc agctgctttt tgcctgtact	2160
gggtctctct gggttagacca gatctgagcc tgggagctct ctggctaact agagaaccca	2220
ctgcttaagc ctcaataaag cttctagaga tccctcgacc tcgagatcca ttgtgctggc	2280
gcggattctt tatcactgat aagttggtgg acatattatg tttatcagtg ataaagtgtc	2340
aagcatgaca aagttgcagc cgaatacagt gatccgtgcc gccctagacc tgttgaacga	2400
ggtcggcgta gacggtctga cgacacgcaa actggcgga cggttggggg ttcagcagcc	2460
ggcgctttac tggcacttca ggaacaagcg ggcgctgtct gacgcactgg ccgaagccat	2520
gctggcgag aatcatagca cttcgggtcc gagagccgac gacgactggc gctcatttct	2580
gactgggaat gcccgagct tcaggcaggc gctgctgcgc taccgccagc acaatggatc	2640
tcgagggatc ttccatacct accagttctg cgctgcagg tcgcgccgc gactctagag	2700
gatctttgtg aaggaacctt acttctgtgg tgtgacataa ttggacaaac tacctacaga	2760
gatttaaagc tctaaggtaa atataaaatt ttaagtgtg taatgtgtta aactactgat	2820
tctaattgtt tgtgtatttt agattccaac ctatggaact gatgaatggg agcagtggtg	2880
gaatgccttt aatgaggaaa acctgttttg ctcaagaaga atgccatcta gtgatgatga	2940
ggctactgct gactctcaac attctactcc tccaaaaaag aagagaaagg tagaagacc	3000
caaggacttt ctttcagaat tgctaagttt tttgagtcac gctgtgttta gtaatagaac	3060
tcttgcttgc tttgctattt acaccacaaa ggaaaaagct gactgtctat acaagaaaaat	3120
tatggaaaaa tattctgtaa cttttataag taggcataac agttataatc ataacatact	3180
gttttttctt actccacaca ggcataagat gtctgtctatt aataactatg ctcaaaaatt	3240
gtgtaccttt agctttttaa tttgtaaaag ggttaataag gaatatttga tgtatagtgc	3300
cttgactaga gatcataatc agccatacca cattttaga ggttttactt gctttaaaaa	3360
acctcccaca cttccccctg aacctgaaac ataaaatgaa tgcaattgtt gttgttaact	3420
tgtttattgc agcttataat ggttacaaat aaagcaatag catcacaaat ttcacaaata	3480
aagcattttt ttcactgcac tctagttgtg gtttgtccaa actcatcaat gtatcttacc	3540
atgtctggat cctgtggaat gtgtgtcagt taggggtgtg aaagtcccca ggctccccag	3600
caggcagaag tatgcaaagc atgcatctca attagtcagc aaccaggtgt ggaagtccc	3660
caggctcccc agcaggcaga agtatgcaaa gcatgcatct caattagtca gcaaccatag	3720

11-88L.ST25.txt

tccccgccct aactccgccc atccccgccc taactccgcc cagttccgcc cattctccgc 3780
 cccatggctg actaattttt ttattttatg cagaggccga ggccgcctcg gcctctgagc 3840
 tattccagaa gtatgtgagga ggcttttttg gaggcctagg cttttgcaaa aagctaattc 3900

<210> 7
 <211> 1514
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (100)..(759)

<400> 7
 agactctcag gccttggcag gtgcgtcttt cagttccctt cacacttcgg gttcctcggg 60
 gaggaggggc tggaacccta gcccatcgtc aggacaaag atg ctc agg ctg ctc 114
 Met Leu Arg Leu Leu
 1 5
 ttg gct ctc aac tta ttc cct tca att caa gta aca gga aac aag att 162
 Leu Ala Leu Asn Leu Phe Pro Ser Ile Gln Val Thr Gly Asn Lys Ile
 10 15 20
 ttg gtg aag cag tcg ccc atg ctt gta gcg tac gac aat gcg gtc aac 210
 Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr Asp Asn Ala Val Asn
 25 30 35
 ctt agc tgc aag tat tcc tac aat ctc ttc tca agg gag ttc cgg gca 258
 Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser Arg Glu Phe Arg Ala
 40 45 50
 tcc ctt cac aaa gga ctg gat agt gct gtg gaa gtc tgt gtt gta tat 306
 Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu Val Cys Val Val Tyr
 55 60 65
 ggg aat tac tcc cag cag ctt cag gtt tac tca aaa acg ggg ttc aac 354
 Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser Lys Thr Gly Phe Asn
 70 75 80 85
 tgt gat ggg aaa ttg ggc aat gaa tca gtg aca ttc tac ctc cag aat 402
 Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr Phe Tyr Leu Gln Asn
 90 95 100
 ttg tat gtt aac caa aca gat att tac ttc tgc aaa att gaa gtt atg 450
 Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys Lys Ile Gln Val Met
 105 110 115
 tat cct cct cct tac cta gac aat gag aag agc aat gga acc att atc 498
 Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile
 120 125 130
 cat gtg aaa ggg aaa cac ctt tgt tgt cca agt ccc cta ttt ccc gga cct 546
 His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro
 135 140 145
 tct aag ccc ttt tgg gtg ctg gtg gtg gtt ggt gga gtc ctg gct tgc 594
 Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys

11-88L.ST25.txt

```

150                155                160                165
tat agc ttg cta gta aca gtg gcc ttt att att ttc tgg gtg agg agt      642
Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
170
aag agg agc agg ctc ctg cac agt gac tac atg aac atg act ccc cgc      690
Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
185
cgc ccc ggg ccc acc cgc aag cat tac cag ccc tat gcc cca cca cgc      738
Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
200
gac ttc gca gcc tat cgc tcc tgacacggac gcctatccag aagccagccg      789
Asp Phe Ala Ala Tyr Arg Ser
215
gctggcagcc cccatctgct caatatcact gctctggata ggaaatgacc gccatctcca      849
gccggccacc tcagccctgt ttgggccacc aatgccaaatt tttctcgagt gactagacca
909
aatatcaaga tcattttgag actctgaaat gaagtaaaag agatttcctg tgacaggcca
969
agtcctacag tgccatggcc cacattccaa ctaccatgt acttagtgac ttgactgaga
1029
agttagggta gaaaacaaaa agggagtgga ttctgggagc ctctccctt tctcactcac
1089
ctgcacatct cagtcaagca aagtgtgta tccacagaca ttttagttgc agaagaaagg
1149
ctaggaaatc attccttttg gtaaatggg tgtttaattct ttggttagt ggggttaaagc
1209
gggtaagtta gagtggggg agggatagga agacatatat aaaaaccatt aaaacactgt
1269
ctccactca tgaaatgagc cagtagttc ctatttaatg ctgttttcct ttagtttaga
1329
aatacataga cattgtcttt tatgaattct gatcatattt agtcattttg accaaatgag
1389
ggatttggtc aaatgaggga ttccctcaaa gcaatatcag gtaaaccaag ttgctttcct
1449
cactccctgt catgagactt cagtgttaat gtccacaata tactttcgaa agaataaaat
1509
agttc
1514

<210> 8
<211> 220
<212> PRT
<213> Homo sapiens

<400> 8
Met Leu Arg Leu Leu Leu Ala Leu Asn Leu Phe Pro Ser Ile Gln Val
1 5 10 15
Thr Gly Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr
20 25 30
Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser
35 40 45

```

11-88L.ST25.txt

Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu
50 55 60
Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser
65 70 75 80
Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr
85 90 95
Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys
100 105 110
Lys Ile Glu Val Met Tyr Pro Pro Tyr Leu Asp Asn Glu Lys Ser
115 120 125
Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
130 135 140
Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
145 150 155 160
Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
165 170 175
Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
180 185 190
Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
195 200 205
Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
210 215 220

<210> 9
<211> 1665
<212> DNA
<213> Homo sapiens

<400> 9
tagaccaga gaggtctcagc tgcactgcc cggtgggag agctgggtgt ggggaacatg 60
gccgggctc cgaggtcct gctgctgcc ctgcttctgg cgctggctg cggcctgcct 120
ggggccttg ctgccaagg taagagcttc ccaggtctc catggccaca gctccggagc 180
tctccctgcc ccatgagctc agagccccc gtctgagcca cagcacagcc cccaggaagc 240
gggtgggtg ctgagcgcc tccagtgtc tggagctcat ttaagagaag gaaaaagggt 300
ggaccgggtg gggagtggcc ggggtgtcc aggcagggcc gctgcttgg gaggaagaag 360

cccacagtct	cggaacacga	ggacagcacc	tcccccaaca	ccacagccgg	tgcccagatc	420
tgctccatgc	cccgtaaagg	accgtgtctt	tggcgacatg	tcagccctgg	gctgtctcag	480
ggccccacca	tccccaccac	tgccccctgc	agggaggaca	ttctctgtcc	ttctggccag	540
actgatggtg	acagcccagg	tcctcccaga	ggtgcagcag	tcctcccact	gcacgactgt	600
ccccgtggga	gcctccgtca	acatcacctg	ctccaccagc	ggggccctgc	gtgggatcta	660
cctgaggcag	ctcgggccac	agccccaaga	catcatttac	tacgaggacg	gggtgggtgcc	720
cactacggac	agacgggttc	ggggccgcat	cgactttcta	gggtcccagg	acaacctgac	780
tatcaccatg	caccgcctgc	agctgtcgga	cactggcacc	tacacctgcc	aggccatcac	840
ggagggtcaat	gtctacggct	ccggcacccct	ggtctgtgtg	acagaggaaac	agtcccgaag	900
atggcacaga	tgctcggacg	ccccaccaag	ggcctctgcc	ctccctgccc	caccgacagg	960
ctccgccctc	cctgaccgcg	agacagcctc	tgccctccct	gacccgccag	cagcctctgc	1020
cctccctcgc	gccttgccgg	tgatctcctt	cctcctcggg	ctgggccctgg	gggtggcgtg	1080
tggtctggcg	aggacacaga	taaagaaact	gtgtctgtgg	cgggataaga	attcggcggc	1140
atgtgtgtgtg	tacgaggaca	tgctgcacag	ccgtgcacac	acgtgtctct	cccccaacca	1200
gtaccagtga	ccagtgggc	ccctgcacgt	ccgcctgtgt	gtccccccag	cacttctcct	1260
gccccaccat	gccccccacc	ctgccacacc	cctcacccctg	ctgtcctccc	acggctgcag	1320
cagagtttga	agggcccacg	cggtcccagc	tccaagcaga	cacacaggca	gtggccaggc	1380
cccacggtgc	ttctcagtgg	acaatgatgc	ctcctccggg	aagccttccc	tgcccagccc	1440
acgccccac	cgggagggaag	cctgactgtc	ctttggctgc	atctcccgac	catggccaag	1500
gagggctttt	ctgtgggatg	ggcctggcac	gcggccctct	cctgtcagtg	ccggcccacc	1560
caccagcagg	cccccaacc	ccaggcagcc	cggcagagg	cgggaggaga	ccagtcccc	1620
accacgccgt	accagaaata	aaggcttctg	tgcttcaaaa	aaaaa		1665

<210> 10
 <211> 2290
 <212> DNA
 <213> Homo sapiens

<400> 10	cccaaagtct	tcagaatgta	tgctccagaa	acctgtggct	gcttcaacca	ttgacagt	60
	tgctgtctgt	ggcttctgca	gacagtcaag	ctgcagctcc	cccaaaggct	gtgtgaaac	120
	ttgagcccc	gtggatcaac	gtgtccagg	aggactctgt	gactctgaca	tgccagggg	180
	ctgcagccc	tgagagcgac	tccattcagt	ggttccacaa	tggaatctc	attccaccc	240
	acacgcagcc	cagctacagg	ttcaaggcca	acaacaatga	cagcggggag	tacacgtgc	300
	agactggcca	gaccagcctc	agcgaccctg	tgcatctgac	tggtcttccc	gaatggctgg	360

tgctccagac	ccctcacctg	gagttccagg	agggagaaac	catcatgctg	agggtgccaca	420
gctggaagga	caagcctctg	gtcaagggtca	cattcttcca	gaatggaaaa	tcccagaaat	480
tctccggtt	ggatcccacc	ttctccatcc	cacaagcaaa	ccacagtcac	agtgggtgatt	540
accactgcac	aggaacaata	ggctacacgc	tggttctatc	caagcctgtg	accatcactg	600
tccaagtgcc	cagcatgggc	agctcttcac	caatggggat	cattgtggct	gtggtcattg	660
cgactgctgt	agcagccatt	gttctgtctg	tagtggcctt	gatctactgc	agggaaaagc	720
ggatttcagc	caattccact	gatcctgtga	aggctgcccc	atttgagcca	cctggagctc	780
aaatgattgc	catcagaaag	agacaacttg	aagaaaccaa	caatgactat	gaaacagctg	840
acggcggtta	catgactctg	aaccccaggg	cacctactga	cgatgataaa	aacatctacc	900
tgactcttcc	tcccacgac	catgtcaaca	gtaataacta	aagagtaacg	ttatgccatg	960
tggtcatact	ctcagcttgc	tgagtggatg	acaaaaagag	gggaattgtt	aaaggaaaat	1020
ttaaatggag	actggaaaaa	tcctgagcaa	acaaaaccac	ctggccctta	gaaatagctt	1080
taactttgct	taaactacaa	acacaagcaa	aacttcacgg	ggtcatacta	catacaagca	1140
taagcaaaac	ttaacttgga	tcatttctgg	taaatgctta	tgtagaaaat	aagacaaccc	1200
cagccaatca	caagcagcct	actaacatat	aattaggtga	ctagggactt	tctaagaaga	1260
tacctacccc	caaaaaacaa	ttatgtaatt	gaaaaccaac	cgattgcctt	tattttgctt	1320
ccacatttcc	ccaataaata	cttgccctgtg	acattttgcc	actggaacac	taaacttcat	1380
gaattgcgcc	tcagattttt	cctttaacat	cttttttttt	tttgacagag	tctcaatctg	1440
ttaccagggc	tggagtgcag	tgggtctatc	ttggctcact	gcaaacccgc	ctcccagggt	1500
taagcgattc	tcattgcctca	gcctcccagt	agctgggatt	agaggcatgt	gccatcatat	1560
ccagctaatt	tttgattttt	ttattttttt	tttttagtag	agacaggggt	tcgcaatggt	1620
ggccaggccg	atctcgaact	tctggcctct	agcgatctgc	ccgcctcggc	ctccccaaagt	1680
gctgggatga	ccagcatcag	ccccaatgtc	cagcctcttt	aacatcttct	ttctctatgcc	1740
ctctctgtgg	atccctactg	ctggttttctg	ccttctccat	gctgagaaca	aaatcaccta	1800
ttcactgctt	atgcagtcgg	aagctccaga	agaacaaaga	gccaatttac	cagaaccaca	1860
ttaagtctcc	attgttttgc	cttgggattt	gagaagagaa	ttagagaggt	gaggatctgg	1920
tatttctctg	actaaattcc	ccttggggaa	gacgaaggga	tgctgcagtt	ccaaaagaga	1980
aggactcttc	cagagtcatc	tacctgagtc	ccaaagctcc	ctgtcctgaa	agccacagac	2040
aatatgggtc	caaatgactg	actgcacctt	ctgtgcctca	gccgttcttg	acatcaagaa	2100
tcttctgttc	catatccaca	cagccaatac	aattagtcaa	accactgtta	ttacagatg	2160
tagcaacatg	agaaacgctt	atgttacagg	ttacatgaga	gcaatcatgt	aagtctatat	2220
gacttcagaa	atgttaaaat	agactaacct	ctaacaacaa	attaaaagtg	attgtttcaa	2280

11-88L.ST25.txt

ggtgaaaaaa

2290

<210> 11
 <211> 1474
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (94)..(984)

<400> 11
 aaagacaaac tgcacccact gaactccgca gctagcatcc aaatcagccc ttgagatttg 60
 aggccttggg gactcaggag ttttgagagc aaa atg aca aca ccc aga aat tca 114
 Met Thr Thr Pro Arg Asn Ser
 1 5
 gta aat ggg act ttc ccg gca gag cca atg aaa ggc cct att gct atg 162
 Val Asn Gly Thr Phe Pro Ala Glu Pro Met Lys Gly Pro Ile Ala Met
 10 15 20
 caa tct ggt cca aaa cca ctc ttc agg agg atg tct tca ctg gtg ggc 210
 Gln Ser Gly Pro Lys Pro Leu Phe Arg Arg Met Ser Leu Val Gly
 25 30 35
 ccc acg caa agc ttc ttc atg agg gaa tct aag act ttg ggg gct gtc 258
 Pro Thr Gln Ser Phe Phe Met Arg Glu Ser Lys Thr Leu Gly Ala Val
 40 45 50 55
 cag att atg aat ggg ctc ttc cac att gcc ctg ggg ggt ctt ctg atg 306
 Gln Ile Met Asn Gly Leu Phe His Ile Ala Leu Gly Gly Leu Leu Met
 60 65 70
 atc cca gca ggg atc tat gca ccc atc tgt gtg act gtg tgg tac cct 354
 Ile Pro Ala Gly Ile Tyr Ala Pro Ile Cys Val Thr Val Trp Tyr Pro
 75 80 85
 ctc tgg gga ggc att atg tat att att tcc gga tca ctc ctg gca gca 402
 Leu Trp Gly Gly Ile Met Tyr Ile Ile Ser Gly Ser Leu Leu Ala Ala
 90 95 100
 acg gag aaa aac tcc agg aag tgt ttg gtc aaa gga aaa atg ata atg 450
 Thr Glu Lys Asn Ser Arg Lys Cys Leu Val Lys Gly Lys Met Ile Met
 105 110 115
 aat tca ttg agc ctc ttt gct gcc att tct gga atg att ctt tca atc 498
 Asn Ser Leu Ser Leu Phe Ala Ala Ile Ser Gly Met Ile Leu Ser Ile
 120 125 130 135
 atg gac ata ctt aat att aaa att tcc cat ttt tta aaa atg gag agt 546
 Met Asp Ile Leu Asn Ile Lys Ile Ser His Phe Leu Lys Met Glu Ser
 140 145 150
 ctg aat ttt att aga gct cac aca cca tat att aac ata tac aac tgt 594
 Leu Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn Ile Tyr Asn Cys
 155 160 165
 gaa cca gct aat ccc tct gag aaa aac tcc cca tct acc caa tac tgt 642
 Glu Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser Thr Gln Tyr Cys

11-88L.ST25.txt

170 175 180
 tac agc ata caa tct ctg ttc ttg ggc att ttg tca gtg atg ctg atc 690
 Tyr Ser Ile Gln Ser Leu Phe Leu Gly Ile Leu Ser Val Met Leu Ile
 185 190 195
 ttt gcc ttc ttc cag gaa ctt gta ata gct ggc atc gtt gag aat gaa 738
 Phe Ala Phe Phe Gln Glu Leu Val Ile Ala Gly Ile Val Glu Asn Glu
 200 205 210 215
 tgg aaa aga acg tgc tcc aga ccc aaa tct aac ata gtt ctc ctg tca 786
 Trp Lys Arg Thr Cys Ser Arg Pro Lys Ser Asn Ile Val Leu Leu Ser
 220 225 230
 gca gaa gaa aaa aaa gaa cag act att gaa ata aaa gaa gaa gtg gtt 834
 Ala Glu Glu Lys Lys Glu Gln Thr Ile Glu Ile Lys Glu Glu Val Val
 235 240 245
 ggg cta act gaa aca tct tcc caa cca aag aat gaa gaa gac att gaa 882
 Gly Leu Thr Glu Thr Ser Ser Gln Pro Lys Asn Glu Glu Asp Ile Glu
 250 255 260
 att att cca atc caa gaa gag gaa gaa gaa gaa aca gag acg aac ttt 930
 Ile Ile Pro Ile Gln Glu Glu Glu Glu Glu Thr Glu Thr Asn Phe
 265 270 275
 cca gaa cct ccc caa gat cag gaa tcc tca cca ata gaa aat gac agc 978
 Pro Glu Pro Pro Gln Asp Gln Glu Ser Ser Pro Ile Glu Asn Asp Ser
 280 285 290 295
 tct cct taagtgtttt ctctgtttt ctgtttcctt ttttaaacat tagtggtcat 1034
 Ser Pro
 agcttccaag agacatgctg actttcattt cttagaggta tctgcacata cgcaccacat 1094
 ctctatctgg cctttgcatg gaggtagcat agctccttct ctcttacatt gaatgtagag 1154
 aatgtagcca ttgtagcagc ttgtgttgc acgcttcttc ttttagcaaa ctttcttaca 1214
 ctgaagaag gcagaatgag tgcttcagaa tgtgatttcc tactaacctg ttccttggat 1274
 aggcttttta gtatagtatt ttttttgtc attttctcca tcagcaacca gggagactgc 1334
 acctgatgga aaagatatat gactgcttca tgacattcct aaactatctt ttttttattc 1394
 cacatctacg tttttgttg agtccctttt tatcatcctt aaaacaatga tgcaaaaggg 1454
 ctttagagca caatggatct 1474
 <210> 12
 <211> 297
 <212> PRT
 <213> Homo sapiens
 <400> 12
 Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro
 1 5 10 15
 Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg

Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu
 35 40 45
 Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe His Ile
 50 55 60
 Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala Pro Ile
 65 70 75 80
 Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Ile Met Tyr Ile Ile
 85 90 95
 Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu
 100 105 110
 Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile
 115 120 125
 Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser
 130 135 140
 His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro
 145 150 155 160
 Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn
 165 170 175
 Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly
 180 185 190
 Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile
 195 200 205
 Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys
 210 215 220
 Ser Asn Ile Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile
 225 230 235 240
 Glu Ile Lys Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro
 245 250 255
 Lys Asn Glu Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu Glu
 260 265 270

11-88L.ST25.txt

Glu Glu Thr Glu Thr Asn Phe Pro Glu Pro Pro Gln Asp Gln Glu Ser
 275 280 285

Ser Pro Ile Glu Asn Asp Ser Ser Pro
 290 295

<210> 13
 <211> 1888
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (13)..(1608)

<400> 13
 ctccagcctcg ct atg gct ccc agc agc ccc cgg ccc gcg ctg ccc gca ctc 51
 Met Ala Pro Ser Ser Pro Arg Pro Ala Leu Pro Ala Leu
 1 5 10

ctg gtc ctg ctc ggg gct ctg ttc cca gga cct ggc aat gcc cag aca 99
 Leu Val Leu Leu Gly Ala Leu Phe Pro Gly Pro Gly Asn Ala Gln Thr
 15 20 25

tct gtg tcc ccc tca aaa gtc atc ctg ccc cgg gga ggc tcc gtg ctg 147
 Ser Val Ser Pro Ser Lys Val Ile Leu Pro Arg Gly Gly Ser Val Leu
 30 35 40 45

gtg aca tgc agc acc tcc tgt gac cag ccc aag ttg ttg ggc ata gag 195
 Val Thr Cys Ser Thr Ser Cys Asp Gln Pro Lys Leu Leu Gly Ile Glu
 50 55 60

acc ccg ttg cct aaa aag gag ttg ctc ctg cct ggg aac aac cgg aag 243
 Thr Pro Leu Pro Lys Lys Glu Leu Leu Pro Gly Asn Asn Arg Lys
 65 70 75

gtg tat gaa ctg agc aat gtg caa gaa gat agc caa cca atg tgc tat 291
 Val Tyr Glu Leu Ser Asn Val Gln Glu Asp Ser Gln Pro Met Cys Tyr
 80 85 90

tca aac tgc cct gat ggg cag tca aca gct aaa acc ttc ctc acc gtg 339
 Ser Asn Cys Pro Asp Gly Gln Ser Thr Ala Lys Thr Phe Leu Thr Val
 95 100 105

tac tgg act cca gaa cgg gtg gaa ctg gca ccc ctc ccc tct tgg cag 387
 Tyr Trp Thr Pro Glu Arg Val Glu Leu Ala Pro Leu Pro Ser Trp Gln
 110 115 120 125

cca gtg ggc aag aac ctt acc cta cgc tgc cag gtg gag ggt ggg gca 435
 Pro Val Gly Lys Asn Leu Thr Leu Arg Cys Gln Val Glu Gly Gly Ala
 130 135 140

ccc cgg gcc aac ctc acc gtg gtg ctg ctc cgt ggg gag aag gag ctg 483
 Pro Arg Ala Asn Leu Thr Val Val Leu Leu Arg Gly Glu Lys Glu Leu
 145 150 155

aaa cgg gag cca gct gtg ggg gag ccc gct gag gtc acg acc acg gtg 531
 Lys Arg Glu Pro Ala Val Gly Glu Pro Ala Glu Val Thr Thr Thr Val
 160 165 170

11-88L.S125.txt

ctg Leu	gtg Val 175	agg Arg	aga Arg	gat Asp	cac His	cat His 180	gga Gly	gcc Ala	aat Asn	ttc Phe	tgc Gln 185	tgc Cys	cgc Arg	act Thr	gaa Glu	579
ctg Leu 190	gac Asp	ctg Leu	cgg Arg	ccc Pro	caa Gln 195	ggg Gly	ctg Leu	gag Glu	ctg Leu	ttt Phe 200	gag Glu	aac Asn	acc Thr	tgc Ser	gcc Ala 205	627
ccc Pro	tac Tyr	cag Gln	ctc Leu	cag Gln 210	acc Thr	ttt Phe	gtc Val	ctg Leu	cca Pro 215	gcg Ala	act Thr	ccc Pro	cca Pro	caa Gln 220	ctt Leu	675
gtc Val	agc Ser	ccc Pro	cgg Arg 225	gtc Val	cta Leu	gag Glu	gtg Val	gac Asp 230	acg Thr	cag Gln	ggg Gly	acc Thr	gtg Val 235	gtc Val	tgt Cys	723
tcc Ser	ctg Leu	gac Asp 240	ggg Gly	ctg Leu	ttc Phe	cca Pro	gtc Val 245	tcg Ser	gag Glu	gcc Ala	cag Gln	gtc Val 250	cac His	ctg Leu	gca Ala	771
ctg Leu 255	ggg Gly	gac Asp	cag Gln	agg Arg	ttg Leu	aac Asn 260	ccc Pro	aca Thr	gtc Val	acc Thr	tat Tyr 265	ggc Gly	aac Asn	gac Asp	tcc Ser	819
ttc Phe 270	tgc Ser	gcc Ala	aag Lys	gcc Ala	tca Ser 275	gtc Val	agt Ser	gtg Val	acc Thr	gca Ala 280	gag Glu	gac Asp	gag Glu	ggc Gly	acc Thr 285	867
cag Gln	cgg Arg	ctg Leu	acg Thr	tgt Cys 290	gca Ala	gta Val	ata Ile	ctg Leu	ggg Gly 295	aac Asn	cag Gln	agc Ser	cag Gln	gag Glu 300	aca Thr	915
ctg Leu	cag Gln	aca Thr	gtg Val 305	acc Thr	atc Ile	tac Tyr	agc Ser	ttt Phe 310	ccg Pro	gcg Ala	ccc Pro	aac Asn 315	gtg Val 315	att Ile	ctg Leu	963
acg Thr	aag Lys	cca Pro 320	gag Glu	gtc Val	tca Ser	gaa Glu	ggg Gly 325	acc Thr	gag Glu	gtg Val	aca Thr	gtg Val 330	aag Lys	tgt Cys	gag Glu	1011
gcc Ala	cac His 335	cct Pro	aga Arg	gcc Ala	aag Lys	gtg Val 340	acg Thr	ctg Leu	aat Asn	ggg Gly	gtt Val 345	cca Pro	gcc Ala	cag Gln	cca Pro	1059
ctg Leu 350	ggc Gly	ccg Pro	agg Arg	gcc Ala	cag Gln 355	ctc Leu	ctg Leu	ctg Leu	aag Lys	gcc Ala 360	acc Thr	cca Pro	gag Glu	gac Asp	aac Asn 365	1107
ggg Gly	cgc Arg	agc Ser	ttc Phe	tcc Ser 370	tgc Cys	tct Ser	gca Ala	acc Thr	ctg Leu 375	gag Glu	gtg Val	gcc Ala	ggc Gly	cag Gln 380	ctt Leu	1155
ata Ile	cac His	aag Lys	aac Asn 385	cag Gln	acc Thr	cgg Arg	gag Glu	ctt Leu 390	cgt Arg	gtc Val	ctg Leu	tat Tyr 395	ggc Gly	ccc Pro	cga Arg	1203
ctg Leu	gac Asp	gag Glu 400	agg Arg	gat Asp	tgt Cys	ccg Pro	gga Gly 405	aac Asn	tgg Trp	acg Thr	tgg Trp	cca Pro 410	gaa Glu	aat Asn	tcc Ser	1251
cag Gln 415	cag Gln	act Thr	cca Pro	atg Met	tgc Cys	cag Gln 420	gct Ala	tgg Trp	ggg Gly	aac Asn	cca Pro 425	tgg Leu	ccc Pro	gag Glu	ctc Leu	1299

11-88L.ST25.txt

aag tgt cta aag gat ggc act ttc cca ctg ccc atc ggg gaa tca gtg 1347
Lys Cys Leu Lys Asp Gly Thr Phe Pro Leu Pro Ile Gly Glu Ser Val
430 435 440 445

act gtc act cga gat ctt gag ggc acc tac ctc tgt cgg gcc agg agc 1395
Thr Val Thr Arg Asp Leu Glu Gly Thr Tyr Leu Cys Arg Ala Arg Ser
450 455 460

act caa ggg gag gtc acc cgc gag gtg acc gtg aat gtg ctc tcc ccc 1443
Thr Gln Gly Glu Val Thr Arg Glu Val Thr Val Asn Val Leu Ser Pro
465 470 475

cgg tat gag att gtc atc atc act gtg gta gca gcc gca gtc ata atg 1491
Arg Tyr Glu Ile Val Ile Ile Thr Val Val Ala Ala Val Ile Met
480 485 490

ggc act gca ggc ctc agc acg tac ctc tat aac cgc cag cgg aag atc 1539
Gly Thr Ala Gly Leu Ser Thr Tyr Leu Tyr Asn Arg Gln Arg Lys Ile
495 500 505

aag aaa tac aga cta caa cag gcc caa aaa ggg acc ccc atg aaa ccg 1587
Lys Lys Tyr Arg Leu Gln Gln Ala Gln Lys Gly Thr Pro Met Lys Pro
510 515 520 525

aac aca caa gcc acg cct ccc tgaacctatc ccgggacagg gcctcttcct 1638
Asn Thr Gln Ala Thr Pro Pro
530

cggccttccc atattggtgg cagtgggtgcc aactgaaca gagtgaaga catatgccat 1698
gcagctacac ctaccggccc tgggacgccg gaggacaggg cattgtcctc agtcagatac 1758
aacagcattt ggggccatgg tacctgcaca cctaaaacac taggccacgc atctgatctg 1818
tagtcacatg actaagccaa gaggaaggaa cagcatttgg ggccatggta cctgcacacc 1878
taaaacacta 1888

<210> 14
<211> 532
<212> PRT
<213> Homo sapiens

<400> 14

Met Ala Pro Ser Ser Pro Arg Pro Ala Leu Pro Ala Leu Leu Val Leu
1 5 10 15

Leu Gly Ala Leu Phe Pro Gly Pro Gly Asn Ala Gln Thr Ser Val Ser
20 25 30

Pro Ser Lys Val Ile Leu Pro Arg Gly Gly Ser Val Leu Val Thr Cys
35 40 45

Ser Thr Ser Cys Asp Gln Pro Lys Leu Leu Gly Ile Glu Thr Pro Leu
50 55 60

11-88L.5T25.txt

Pro Lys Lys Glu Leu Leu Leu Pro Gly Asn Asn Arg Lys Val Tyr Glu
 65 70 75 80
 Leu Ser Asn Val Gln Glu Asp Ser Gln Pro Met Cys Tyr Ser Asn Cys
 85 90 95
 Pro Asp Gly Gln Ser Thr Ala Lys Thr Phe Leu Thr Val Tyr Trp Thr
 100 105 110
 Pro Glu Arg Val Glu Leu Ala Pro Leu Pro Ser Trp Gln Pro Val Gly
 115 120 125
 Lys Asn Leu Thr Leu Arg Cys Gln Val Glu Gly Gly Ala Pro Arg Ala
 130 135 140
 Asn Leu Thr Val Val Leu Leu Arg Gly Glu Lys Glu Leu Lys Arg Glu
 145 150 155 160
 Pro Ala Val Gly Glu Pro Ala Glu Val Thr Thr Thr Val Leu Val Arg
 165 170 175
 Arg Asp His His Gly Ala Asn Phe Ser Cys Arg Thr Glu Leu Asp Leu
 180 185 190
 Arg Pro Gln Gly Leu Glu Leu Phe Glu Asn Thr Ser Ala Pro Tyr Gln
 195 200 205
 Leu Gln Thr Phe Val Leu Pro Ala Thr Pro Pro Gln Leu Val Ser Pro
 210 215 220
 Arg Val Leu Glu Val Asp Thr Gln Gly Thr Val Val Cys Ser Leu Asp
 225 230 235 240
 Gly Leu Phe Pro Val Ser Glu Ala Gln Val His Leu Ala Leu Gly Asp
 245 250 255
 Gln Arg Leu Asn Pro Thr Val Thr Tyr Gly Asn Asp Ser Phe Ser Ala
 260 265 270
 Lys Ala Ser Val Ser Val Thr Ala Glu Asp Glu Gly Thr Gln Arg Leu
 275 280 285
 Thr Cys Ala Val Ile Leu Gly Asn Gln Ser Gln Glu Thr Leu Gln Thr
 290 295 300
 Val Thr Ile Tyr Ser Phe Pro Ala Pro Asn Val Ile Leu Thr Lys Pro
 305 310 315 320

11-88L.ST25.txt

Glu Val Ser Glu Gly Thr Glu Val Thr Val Lys Cys Glu Ala His Pro
325 330 335

Arg Ala Lys Val Thr Leu Asn Gly Val Pro Ala Gln Pro Leu Gly Pro
340 345 350

Arg Ala Gln Leu Leu Leu Lys Ala Thr Pro Glu Asp Asn Gly Arg Ser
355 360 365

Phe Ser Cys Ser Ala Thr Leu Glu Val Ala Gly Gln Leu Ile His Lys
370 375 380

Asn Gln Thr Arg Glu Leu Arg Val Leu Tyr Gly Pro Arg Leu Asp Glu
385 390 395 400

Arg Asp Cys Pro Gly Asn Trp Thr Trp Pro Glu Asn Ser Gln Gln Thr
405 410 415

Pro Met Cys Gln Ala Trp Gly Asn Pro Leu Pro Glu Leu Lys Cys Leu
420 425 430

Lys Asp Gly Thr Phe Pro Leu Pro Ile Gly Glu Ser Val Thr Val Thr
435 440 445

Arg Asp Leu Glu Gly Thr Tyr Leu Cys Arg Ala Arg Ser Thr Gln Gly
450 455 460

Glu Val Thr Arg Glu Val Thr Val Asn Val Leu Ser Pro Arg Tyr Glu
465 470 475 480

Ile Val Ile Ile Thr Val Val Ala Ala Ala Val Ile Met Gly Thr Ala
485 490 495

Gly Leu Ser Thr Tyr Leu Tyr Asn Arg Gln Arg Lys Ile Lys Lys Tyr
500 505 510

Arg Leu Gln Gln Ala Gln Lys Gly Thr Pro Met Lys Pro Asn Thr Gln
515 520 525

Ala Thr Pro Pro
530

<210> 15
<211> 1921
<212> DNA
<213> Homo sapiens

<400> 15

ggagagctctg accaccatgc cacctcctcg cctcctcttc tctcctctct tcctcacccc	60
catggaagtc aggcccgagg aacctctatg gtcaagggtg aagagggaga taacgctgtg	120
ctgcagtgcc tcaaggggac ctcatatggc ccactcagc agctgacctg gtctcgggag	180
tccccgtta aacctctctt aaaactcagc ctggggctgc caggcctggg aatccacatg	240
aggccccctg ccattctggt ttctatcttc aacgtgtctc aacagatggg gggcttctac	300
ctgtgccagc cggggccccc ctctgagaag gcctggcagc ctgctgggac agtcaatgtg	360
gagggcagcg gggagctgtt ccggtggaat gtttcggacc taggtggcct gggctgtggc	420
ctgaagaaca ggtgtctaga gggccccagc tccccctcgg ggaagctcat gagcccaag	480
ctgtatgtgt gggccaaaga ccgccttgag atctgggagg gagagcctcc gtgtgtccca	540
ccgagggaca gcctgaacca gagcctcagc caggacctca ccattggcccc tggctccaca	600
ctctggctgt cctgtgggtt accccctgac tctgtgtcca ggggccccct ctctcggacc	660
catgtgcacc ccaaggggccc taagtcatgt ctgagcctag agctgaagga cgatcgcccc	720
gccagagata tgtgggtaat ggagacgggt ctgtgtgtgc cccgggccac agctcaagac	780
gttgaaagt attattgtca cgtggcaac ctgacctgt cattccacct ggagatcact	840
gctcggccag tactatgga ctggtctgtg aggactgggt gctggaaggt ctgagctgtg	900
actttggctt atctgatctt ctgctgtgt tcccttggtg gcattcttca tcttcaaga	960
gccctgtgtc tgaggaggaa aagaaagcga atgactgacc ccaccaggag attcttcaaa	1020
gtgacgctc cccaggaag cgggccccag aaccagtacg ggaacgtgct gtctctcccc	1080
acaccacact caggcctcgg acgcgccag cgttgggccc caggcctggg gggcactgcc	1140
ccgtcttatg gaaacccgag cagcgacgtc caggcggatg gagccttggg gtcccggagc	1200
cgcggggagt gggcccgaa gaagaggaag gggagggcta tgaggaacct gacagtggag	1260
aggactccga gttctatgag aacgactcca accttgggca ggaccagctc tcccaggatg	1320
gcagcggtca cgagaacct gaggatgagc ccctgggtcc tgaggatgaa gactccttct	1380
ccaacgtga gtcttatgag aacgaggatg aagagctgac ccagccggtc gccaggacaa	1440
tggaacttct gagcctcat gggctcagct gggacccag ccgggaagca acctccctgg	1500
ggtcccagtc ctatgaggat atgagaggaa tctgtatgc agccccccag ctccgctcca	1560
ttcggggcca gcctggagcc aatcatgagg aagatgcaga ctcttatgag aatctggata	1620
atcccgatgg gccagaccca gcctggggag gagggggccc catgggcacc tggagacca	1680
ggtgatcctc aggtggccag cctggatctc ctcaagtcac caagattcac acctgactct	1740
gaaatctgaa gacctcgagc agatgatgcc aacctctgga gcaatgtgtg ttaggatgtg	1800
tgcatgtgtg taagtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtata catgccagtg	1860
acacttccag tcccccttgt attccttaaa taaactcaat gagctcttcc aaaaaaaaaa	1920

a

1921

```

<210> 16
<211> 1476
<212> DNA
<213> Homo sapiens

<400> 16
acaaagacaa actgcaccca ctgaactccg cagctagcat ccaaatcagc ccttgagatt    60
tgaggccttg gagactcagg agttttgaga gcaaaatgac aacacccaga aattcagtaa    120
atgggaacttt cccggcagag ccaatgaaag gccctattgc tatgcaatct ggtcctaaac    180
cactcttcag gaggatgtct tctactggtg gccccacgca aagcttcttc atgaggggaat    240
ctaagacttt gggggctgtc cagattatga atgggctctt ccacattgcc ctgggggggtc    300
ttctgatgat ccagcagggg atctatgcac ccatctgtgt gactgtgttg taccctctct    360
ggggaggcat tatgtatat atttccggat cactcctggc agcaacggag aaaaactcca    420
ggaagtgttt ggtcaaagga aaaatgataa tgaattcatt gaggctcttt gctgccattt    480
ctggaatgat tctttcaatc atggacatac ttaattattaa aatttcccat ttttataaaa    540
tggagagtct gaattttatt agagctcaca caccatatat taacatatac aactgtgaac    600
cagctaattcc ctctgagaaa aactcccat ctaccaata ctgttacagc atacaatctc    660
tgttcttggg cattttgtca gtgatgctga tctttgcctt ctccaggaa cttgtaaatg    720
ctggcatcgt tgagaatgaa tggaaaagaa cgtgctccag acccaaatct aacatagttc    780
tcctgtcagc agaagaaaaa aaagaacaga ctattgaaat aaaagaagaa gtggttgggc    840
taactgaac atcttcccaa ccaaagaatg aagaagacat tgaaattatt ccaatccaag    900
aagaggaaga agaagaaaca gagacgaact ttccagaacc tcccaagat caggaatcct    960
caccaataga aaatgacagc tctccttaag tgatttcttc tgtttctctg ttcctttttt   1020
aaacattagt gttcatagct tccaagagac atgctgactt tcatttcttg aggtactctg   1080
cacatacgca ccacatctct atctggcctt tgcattggagt gaccatagct ccttctctct   1140
tacattgaat gtagagaatg tagccattgt agcagcttgt gttgtcagc tcttctcttt   1200
gagcaacttt ctacactga agaaaggcag aatgagtgtc tcagaatgtg atttctact   1260
aacctgttcc ttggataggc tttttagtat agtatttttt ttgtcattt tctccatcag   1320
caaccaggga gactgcacct gatggaaaag atatatgact gcttcagac attcctaaac   1380
tatctttttt ttattccaca tctacgtttt tggtagagtc ctttttatc atccttaaaa   1440
caatgatgca aaagggcttt agagcacaat ggaatct   1476

<210> 17
<211> 2290

```

<212> DNA
 <213> Homo sapiens

<400> 17
 cccaaatgtc tcagaatgta tgtcccagaa acctgtggct gcttcaacca ttgacagtgtt 60
 tgtgtctgct ggcttctgca gacagtcaag ctgcagctcc cccaaaggct gtgctgaaac 120
 ttgagccccc gtggatcaac gtgtccagg aggactctgt gactctgaca tgccagggggg 180
 ctgcagagccc tgagagcgac tccattcagt ggttccacaa tgggaatctc attcccaccc 240
 acacgcagcc cagctacagg ttcaaggcca acaacaatga cagcggggag tacacgtgcc 300
 agactggcca gaccagcctc agcgaccctg tgcattctgac tgtgtcttcc gaatggctgg 360
 tgtccagac ccctcacctg gaggttccagg agggagaaa catcatgctg aggtgccaca 420
 gctggaagga caagcctctg gtcaaggcca cattcttcca gaattgaaaa tcccagaaat 480
 tctcccgttt ggatccacc ttctccatcc cacaagcaaa ccacagtcac agtggtgatt 540
 accactgcac aggaaacata ggctacacgc tgttctcacc caagcctgtg accatcactg 600
 tccaagtgcc cagcatgggc agctcttcac caatggggat cattgtggct gtggtcattg 660
 cgactgtgt agcagccatt gttgtgtctg tagtggcctt gatctactgc aggaaaaagc 720
 ggatttcagc caattccact gatctgtga aggtgcccc atttgagcca cctggacgtc 780
 aatgattgc catcagaaa agacaacttg aagaaccaa caatgactat gaaacagctg 840
 acggcggtc catgactctg aaccccaggg cacctactga cgatgataaa aacatctacc 900
 tgactcttcc tcccacagac catgtcaaca gtaataacta aagagtaacg ttatgccatg 960
 tggtcatact ctgactgtgc tgagtggatg acaaaaagag gggaaattgt aaaggaaaat 1020
 ttaaatggag actggaaaaa tcctgagcaa acaaaaccac ctggccctta gaaatagctt 1080
 taactttgct taaactacaa acacaagcaa aacttcacgg ggtcatacta catacaagca 1140
 taagcaaaac ttaacttgga tcatttctgg taaatgctta tgttagaaat aagacaacc 1200
 cagccaatca caagcagcct actaacatat aattaggatg ctagggactt tctaagaaga 1260
 tacctacccc caaaaaacaa ttatgtaatt gaaaaccaac cgattgcctt tattttgctt 1320
 ccacattttc ccaataaata ctgacctgtg acattttgcc actggaacac taaacttcac 1380
 gaattgcgcc tcagattttt ctttaacat cttttttttt ttgacagag tctcaatctg 1440
 ttaccaggcg tggagtgcag tgggtctatc ttggctcact gcaaaccgcg ctcccagggtt 1500
 taagcgattc tcatgcctca gcctcccagt agctgggatt agaggcatgt gccatcatac 1560
 ccagctaatt ttgtattttt ttattttttt tttttagtag agacaggggtt tcgcaatggt 1620
 ggccaggccg atctcgaact tctggcctct agcgatctgc ccgctcggc ctcccgaagt 1680
 gctgggatga ccagcatcag ccccaatgtc cagcctcttt aacatcttct ttctatgcc 1740
 ctctctgtgg atccctactg ctggtttctg cttctccat gctgagaaca aaatcaccta 1800

11-88L.ST25.txt

ttcactgctt atgcagtcgg aagctccaga agaacaaga gcccaattac cagaaccaca	1860
ttaagctccc attgttttgc cttgggattt gagaagagaa ttagagaggt gaggatctgg	1920
tatttccctg actaaattcc cttggggaa gacgaaggga tgctgcagtt ccaaaagaga	1980
aggactcttc cagagtcac tacctgagtc ccaaagctcc ctgtcctgaa agccacagac	2040
aatatggtcc caaatgactg actgcacctt ctgtgcctca gccgttcttg acatcaagaa	2100
tcttctgttc cacatccaca cagccaatac aattagtcaa accactgtta ttaacagatg	2160
tagcaacatg agaaacgctt atgttacagg ttacatgaga gcaatcatgt aagtcctat	2220
gacttcagaa atgttaaaat agactaacct ctaacaacaa attaaaagtg attgtttcaa	2280
ggtgaaaaaa	2290

<210> 18
 <211> 2171
 <212> DNA
 <213> Homo sapiens

<400> 18	
gctgtgactg ctgtgctctg ggcgccactc gctccaggga gtgatgggaa tcctgtcatt	60
cttacctgtc cttgccactg agagtgactg ggctgactgc aagtcctccc agccttgggg	120
tcatatgctt ctgtggacag ctgtgctatc cctggctcct gttgctggga cactgcagc	180
tccccaaag gctgtgtgta aactcgagcc ccagtggatc aacgtgctcc aggaggactc	240
tgtagctctg acatgccggg ggactcacag ccttgagagc gactccattc agtggttcca	300
caatgggaat ctatttccca cccacacgca gccagctac aggttcaagg ccaacaacaa	360
tgacagcggg gagtacacgt gccagactgg ccagaccagc ctacagcacc ctgtgcatct	420
gactgtgctt tctggtcagt ggaggaaggc cccaggggtg acctggggagg gccaggacgg	480
atgaaatctg ctttcaggca gaggtttgca ggaagggggg gtggcctgct tactgggaa	540
tatcgctgtg agttgccctc gcacatatca gtggtttgtt ttgctcagct tctgattgaa	600
cagaagaagg tttcaaggcc aaaaacaggc agccaagtgt gagagaagca gaaggaaatc	660
cctactgcat aaaaccatt tcatttttaa tggcagaatt gaaaagcaca gaccacaact	720
gaatcctagc cctggaaaatg actcactata caacatgatg aattcattta acccttgagt	780
ttccatttct tcacctgtct cgtggggcac taacgcctcc ctacagaggct tctggtgaga	840
atcagtgctt ccttgcctcc gcccgcctcc ccatgcccct tctccagctt ctactgtgct	900
taggtgtctt tctctgtctt tctcttccac cagcctgtgg gaaacctgag atgaaagtcg	960
tgctttacc atctttgtat ttccagcatc tgaaactggg cagagcttaa taaatatttt	1020
gctggagagg ttgatgatg tacaagctc ccattgaaag gtggctctct gtaaagcaaa	1080
gttacaatga gattgtgatg aacattgtcc ttgtggcttt tcaacttagc cctcccttc	1140

11-88L.ST25.txt

```

acctgaagag caaatTTTCC tcaaaagtac acagcaaacg aatgaccacac ttgtgacact 1200
gttgccTTta gacctgctg gaaagaagct ccacatttat taacattccc gaagtaaatt 1260
tatcaggtag cattcatcag gtaacatttg ttgcacattc atgacttttc tactgtccac 1320
aaaggcatat gtccttatca tatgcggact cctcgggtcac actggattct tccttccctc 1380
ctcgacatgg aagagatggc atcttagggg ctcttggtgt ctctctgcag aggcctgtcg 1440
ggcaggaaaa ggctgcagct gccttctctg gagaaggagg agatgagtgat atcctgaaca 1500
cctattatgt gctaggggct attgtagata catgacacta tcatgctcat ttctacgaat 1560
gaggaaactg aggcctcagaa gacttaaatt atttgcccaa gaggatataaa tgacagagcc 1620
agcattagag tccaggactg tctgatttca gacctaaagct gttccctctg cacatcgtgt 1680
ccccaccgta aggaagatct gggctctcaga gctgagccaa gacctcccg gtctctctgcg 1740
gtttttttgt tctttcagag tggctggtgc tccagacccc tcacctggag ttccaggagg 1800
gagaaacat cggtgctgag tgccacagct ggaaggacaa gcctctggtc aagggtcacat 1860
tcttccagaa tggaaaatcc aagaaatttt cccgttcgga tcccaacttc tccatccac 1920
aagcaaacca cagtcacagt ggtgattacc actgcacagg aaacataggg tacacgctgt 1980
actcatcCaa gcctgtgacc atcactgtcc aagctcccag ctcttcaccg atggggatca 2040
ttgtggctgt ggtcactggg attgctgtag cggccattgt tgctgctgta gtggccttga 2100
tctactgcag gaaaaagcgg atttcagggt tgtagctcct cccggtccct ttgttatca 2160
gtttccactt t 2171

```

```

<210> 19
<211> 1004
<212> DNA
<213> Homo sapiens

```

```

<400> 19
gcctcgtctg ggcgccaggt ggtcctgccg cctggtctca cctcgccatg gttcgtctgc 60
ctctgcagtg cgtcctctgg ggctgcttgc tgaccgctgt ccattccagaa cccccactg 120
catgcagaga aaaacagtac ctaataaaca gtcagtgtgt ttctttgtgc cagccaggac 180
agaaactggt gagtgactgc acagagttca ctgaaacgga atgccttcct tgccggtgaaa 240
gcgaattcct agacacctgg aacagagaga cacactgccA ccagcacaaa tactgcgacc 300
ccaacctagg gcttcgggtc cagcagaagg gcacctcaga aacagacacc atctgcacct 360
gtgaagaagg ctggcaactgt acgagtgagg cctgtgagag ctgtgtctctg caccgctcat 420
gtctgcccgg ctttggggct aagcagattg ctacaggggg ttctgatacc atctgcgagc 480
cctgcccagt cggcttcttc tccaatgtgt catctgcttt cgaaaaatgt cacccttgga 540
caagctgtga gaccaaaagc ctggttgtgc aacaggcagg cacaacaag actgatgtg 600

```

11-88L.ST25.txt

```

tctgtggtcc ccaggatcgg ctgagagccc tgggtggtgat ccccatcatc ttcgggatcc 660
tgtttgccat cctcttggtg ctggtcttta tcaaaaagggt ggccaagaag ccaaccaata 720
aggcccccca ccccaagcag gaaccccagg agatcaattt tcccagcagat cttcctggct 780
ccaacactgc tgctccagtg caggagactt tacatggatg ccaaccggtc acccaggagg 840
atggcaaaga gagtgcgac tcagtgcagg agagacagtg aggtgcacc caccaggagg 900
tgtggccacg tgggcaaaca ggcagttggc cagagagcct ggtgctgctg ctgcaggggg 960
gcaggcagaa gcggggagct atgcccagtc agtgccagcc cctc 1004

```

```

<210> 20
<211> 1870
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (211)..(1626)

```

```

<400> 20
gaaaaatcct tcttagccat ttaaagata gctttccaat gattagacga attgattctt 60
tctgtgactc atcagttctt ttcctgtaaa attcatgtct tgctgttgat ttgtgaataa 120
gaaccagagc ttgtagaaac cactttaatc atatccagga gtttgcaaga aacaggtgct 180
taacactaat tcacctcctg aacaagaaaa atg ggc tgt gac cgg aac tgt ggg 234
Met Gly Cys Asp Arg Asn Cys Gly
1 5
ctc atc gct ggg gct gtc att ggt gct gtc ctg gct gtg ttt gga ggt 282
Leu Ile Ala Gly Ala Val Ile Gly Ala Val Leu Ala Val Phe Gly Gly
10 15 20
att cta atg cca gtt gga gac ctg ctt atc cag aag aca att aaa aag 330
Ile Leu Met Pro Val Gly Asp Leu Leu Ile Gln Lys Thr Ile Lys Lys
25 30 35 40
caa gtt gtc ctc gaa gaa ggt aca att gct ttt aaa aat tgg gtt aaa 378
Gln Val Val Leu Glu Glu Gly Thr Ile Ala Phe Lys Asn Trp Val Lys
45 50 55
aca ggc aca gaa gtt tac aga cag ttt tgg atc ttt gat gtg caa aat 426
Thr Gly Thr Glu Val Tyr Arg Gln Phe Trp Ile Phe Asp Val Gln Asn
60 65 70
cca cag gaa gtg atg atg aac agc agc aac att caa gtt aag caa aga 474
Pro Gln Glu Val Met Met Asn Ser Ser Asn Ile Gln Val Lys Gln Arg
75 80 85
ggt cct tat acg tac aga gtt cgt ttt cta gcc aag gaa aat gta acc 522
Gly Pro Tyr Thr Tyr Arg Val Arg Phe Leu Ala Lys Glu Asn Val Thr
90 95 100
cag gac gct gag gac aac aca gtc tct ttc ctg cag ccc aat ggt gcc 570
Gln Asp Ala Glu Asp Asn Thr Val Ser Phe Leu Gln Pro Asn Gly Ala

```

11-88L.ST25.txt

105	110	115	120	
atc ttc gaa cct tca cta tca gtt gga aca gag gct gac aac ttc aca Ile Phe Glu Pro Ser 125 Leu Ser Val Gly Thr 130 Glu Ala Asp Asn Phe Thr				618
gtt ctc aat ctg gct gtg gca gct gca tcc cat atc tat caa aat caa Val Leu Asn Leu 140 Ala Val Ala Ala Ser His Ile Tyr Gln Asn Gln				666
ttt gtt caa atg atc ctc aat tca ctt att aac aag tca aaa tct tct Phe Val Gln Met Ile Leu Asn Ser 160 Leu Ile Asn Lys Ser Lys Ser Ser				714
atg ttc caa gtc aga act ttg aga gaa ctg tta tgg ggc tat agg gat Met Phe Gln Val Arg Thr Leu 175 Arg Glu Leu Leu Trp 180 Gly Tyr Arg Asp				762
cca ttt ttg agt ttg gtt ccg tac cct gtt act acc aca gtt ggt ctg Pro Phe Leu Ser Leu 190 Val Pro Tyr Pro Val Thr 195 Thr Thr Val Gly Leu 200				810
ttt tat cct tac aac aat act gca gat gga gtt tat aaa gtt ttc aat Phe Tyr Pro Tyr Asn 205 Asn Thr Ala Asp Gly Val Tyr Lys Val Phe Asn 215				858
gga aaa gat aac ata agt aaa gtt gcc ata atc gac aca tat aaa ggt Gly Lys Asp Asn 220 Ile Ser Lys Val Ala 225 Ile Ile Asp Thr Tyr Lys Gly				906
aaa agg aat ctg tcc tat tgg gaa agt cac tgc gac atg att aat ggt Lys Arg Asn Leu Ser Tyr Trp Glu 240 Ser His Cys Asp Met Ile Asn Gly 245				954
aca gat gca gcc tca ttt cca cct ttt gtt gag aaa agc cag gta ttg Thr Asp Ala Ala Ser Phe 255 Pro Pro Val Glu Lys 260 Ser Gln Val Leu				1002
cag ttc ttt tct tct gat att tgc agg tca atc tat gct gta ttt gaa Gln Phe Phe Ser Ser Asp 270 Ile Cys Arg Ser Ile Tyr Ala Val Phe Glu 280				1050
tcc gac gtt aat ctg aaa gga atc cct gtg tat aga ttt gtt ctt cca Ser Asp Val Asn Leu 285 Lys Gly Ile Pro Val Tyr Arg Phe Val Leu Pro 295				1098
tcc aag gcc ttt gcc tct cca gtt gaa aac cca gac aac tat tgt ttc Ser Lys Ala Phe 300 Ala Ser Pro Val Glu 305 Asn Pro Asp Asn Tyr Cys Phe 310				1146
tgc aca gaa aaa att atc tca aaa aat tgt aca tca tat ggt gtg cta Cys Thr Glu Lys Ile Ile Ser Lys 320 Asn Cys Thr Ser Tyr 325 Gly Val Leu				1194
gac atc agc aaa tgc aaa gaa ggg aga cct gtg tac att tca ctt cct Asp Ile Ser Lys Cys Lys Glu 335 Gly Arg Pro Val Tyr 340 Ile Ser Leu Pro				1242
cat ttt ctg tat gca agt cct gat gtt tca gaa cct att gat gga tta His Phe Leu Tyr Ala Ser 350 Pro Asp Val Ser Glu 355 Pro Ile Asp Gly Leu 360				1290
aac cca aat gaa gaa gaa cat agg aca tac ttg gat att gaa cct ata				1338

11-88L.ST25.txt

```

Asn Pro Asn Glu Glu Glu His Arg Thr Tyr Leu Asp Ile Glu Pro Ile
365 370 375
act gga ttc act tta caa ttt gca aaa cgg ctg cag gtc aac cta ttg 1386
Thr Gly Phe Thr Leu Gln Phe Ala Lys Arg Leu Gln Val Asn Leu Leu
380 385 390
gtc aag cca tca gaa aaa att caa gta tta aag aat ctg aag agg aac 1434
Val Lys Pro Ser Glu Lys Ile Gln Val Leu Lys Asn Leu Lys Arg Asn
395 400 405
tat att gtg cct att ctt tgg ctt aat gag act ggg acc att ggt gat 1482
Tyr Ile Val Pro Ile Leu Trp Leu Asn Glu Thr Gly Thr Ile Gly Asp
410 415 420
gag aag gca aac atg ttc aga agt caa gta act gga aaa ata aac ctc 1530
Glu Lys Ala Asn Met Phe Arg Ser Gln Val Thr Gly Lys Ile Asn Leu
425 430 435
ctt ggc ctg ata gaa atg atc tta ctc agt gtt ggt gtg gtg atg ttt 1578
Leu Gly Leu Ile Glu Met Ile Leu Leu Ser Val Gly Val Val Met Phe
445 450 455
gtt gct ttt atg att tca tat tgt gca tgc aga tcg aaa aca ata aaa 1626
Val Ala Phe Met Ile Ser Tyr Cys Ala Cys Arg Ser Lys Thr Ile Lys
460 465 470

taagtatgta ccaaaaaata ttgcttcaat aatattagct tatatattac ttgttttcac 1686
tttatcaaag agaagttaca tattaggcca tatatatttc tagacatgtc tagccactga 1746
tcatttttaa atataggttaa ataaacctat aaatattatc acgcagatca ctaaagtata 1806
tccttaattc tgggagaaaa gagataaaaag atgtacttgt gaccattgta acaatagcac 1866
aaat 1870

<210> 21
<211> 472
<212> PRT
<213> Homo sapiens

<400> 21
Met Gly Cys Asp Arg Asn Cys Gly Leu Ile Ala Gly Ala Val Ile Gly
1 5 10 15
Ala Val Leu Ala Val Phe Gly Gly Ile Leu Met Pro Val Gly Asp Leu
20 25 30
Leu Ile Gln Lys Thr Ile Lys Lys Gln val val Leu Glu Glu Gly Thr
35 40 45
Ile Ala Phe Lys Asn Trp Val Lys Thr Gly Thr Glu val Tyr Arg Gln
50 55 60
Phe Trp Ile Phe Asp Val Gln Asn Pro Gln Glu Val Met Met Asn Ser
65 70 75 80

```

11-88L.ST25.txt

Ser Asn Ile Gln Val Lys Gln Arg Gly Pro Tyr Thr Tyr Arg Val Arg
85 90 95

Phe Leu Ala Lys Glu Asn Val Thr Gln Asp Ala Glu Asp Asn Thr Val
100 105 110

Ser Phe Leu Gln Pro Asn Gly Ala Ile Phe Glu Pro Ser Leu Ser Val
115 120 125

Gly Thr Glu Ala Asp Asn Phe Thr Val Leu Asn Leu Ala Val Ala Ala
130 135 140

Ala Ser His Ile Tyr Gln Asn Gln Phe Val Gln Met Ile Leu Asn Ser
145 150 155 160

Leu Ile Asn Lys Ser Lys Ser Ser Met Phe Gln Val Arg Thr Leu Arg
165 170 175

Glu Leu Leu Trp Gly Tyr Arg Asp Pro Phe Leu Ser Leu Val Pro Tyr
180 185 190

Pro Val Thr Thr Thr Val Gly Leu Phe Tyr Pro Tyr Asn Asn Thr Ala
195 200 205

Asp Gly Val Tyr Lys Val Phe Asn Gly Lys Asp Asn Ile Ser Lys Val
210 215 220

Ala Ile Ile Asp Thr Tyr Lys Gly Lys Arg Asn Leu Ser Tyr Trp Glu
225 230 235 240

Ser His Cys Asp Met Ile Asn Gly Thr Asp Ala Ala Ser Phe Pro
245 250 255

Phe Val Glu Lys Ser Gln Val Leu Gln Phe Phe Ser Ser Asp Ile Cys
260 265 270

Arg Ser Ile Tyr Ala Val Phe Glu Ser Asp Val Asn Leu Lys Gly Ile
275 280 285

Pro Val Tyr Arg Phe Val Leu Pro Ser Lys Ala Phe Ala Ser Pro Val
290 295 300

Glu Asn Pro Asp Asn Tyr Cys Phe Cys Thr Glu Lys Ile Ile Ser Lys
305 310 315 320

Asn Cys Thr Ser Tyr Gly Val Leu Asp Ile Ser Lys Cys Lys Glu Gly

Arg Pro Val Tyr Ile Ser Leu Pro His Phe Leu Tyr Ala Ser Pro Asp
340 345
Val Ser Glu Pro Ile Asp Gly Leu Asn Pro Asn Glu Glu Glu His Arg
355 360
Thr Tyr Leu Asp Ile Glu Pro Ile Thr Gly Phe Thr Leu Gln Phe Ala
370 375
Lys Arg Leu Gln Val Asn Leu Leu Val Lys Pro Ser Glu Lys Ile Gln
385 390 395
Val Leu Lys Asn Leu Lys Arg Asn Tyr Ile Val Pro Ile Leu Trp Leu
405 410
Asn Glu Thr Gly Thr Ile Gly Asp Glu Lys Ala Asn Met Phe Arg Ser
420 425
Gln Val Thr Gly Lys Ile Asn Leu Leu Gly Leu Ile Glu Met Ile Leu
435 440 445
Leu Ser Val Gly Val Val Met Phe Val Ala Phe Met Ile Ser Tyr Cys
450 455 460
Ala Cys Arg Ser Lys Thr Ile Lys
465 470

<210> 22
<211> 1321
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (37)..(1158)

<400> 22
gacagatttc actgctccca ccagcttgga gacaac atg tgg ttc ttg aca act 54
Met Trp Phe Leu Thr 5
1
ctg ctc ctt tgg gtt cca gtt gat ggg caa gtg gac acc aca aag gca 102
Leu Leu Leu Trp Val Pro Val Asp Gly Gln Val Asp Thr Thr Lys Ala 20
10
gtg atc tct ttg cag cct cca tgg gtc agc gtg ttc caa gag gaa acc 150
Val Ile Ser Leu Gln Pro Pro Trp Val Ser Val Phe Gln Glu Glu Thr 35
25 30
gta acc ttg cac tgt gag gtg ctc cat ctg cct ggg agc agc tct aca 198
Page 33

11-88L.ST25.txt

Val	Thr	Leu	His	Cys	Glu	Val	Leu	His	Leu	Pro	Gly	Ser	Ser	Ser	Thr	
40						45					50					
cag	tgg	ttt	ctc	aat	ggc	aca	gcc	act	cag	acc	tgc	acc	ccc	agc	tac	246
Gln	Trp	Phe	Leu	Asn	Gly	Thr	Ala	Thr	Gln	Thr	Ser	Thr	Pro	Ser	Tyr	
55					60				65						70	
aga	atc	acc	tct	gcc	agt	gtc	aat	gac	agt	ggc	gaa	tac	agg	tgc	cag	294
Arg	Ile	Thr	Ser	Ala	Ser	Val	Asn	Asp	Ser	Gly	Glu	Tyr	Arg	Cys	Gln	
				75					80					85		
aga	ggc	ctc	tca	ggg	cga	agt	gac	ccc	ata	cag	ctg	gaa	atc	cac	aga	342
Arg	Gly	Leu	Ser	Gly	Arg	Ser	Asp	Pro	Ile	Gln	Leu	Glu	Ile	His	Arg	
			90					95					100			
ggc	tgg	cta	cta	ctg	cag	gtc	tcc	agc	aga	gtc	ttc	acg	gaa	gga	gaa	390
Gly	Trp	Leu	Leu	Leu	Gln	Val	Ser	Ser	Arg	Val	Phe	Thr	Glu	Gly	Glu	
		105					110					115				
cct	ctg	gcc	ttg	agg	tgt	cat	gcg	tgg	aag	gat	aag	ctg	gtg	tac	aat	438
Pro	Leu	Ala	Leu	Arg	Cys	His	Ala	Trp	Lys	Asp	Lys	Leu	Val	Tyr	Asn	
		120				125					130					
gtg	ctt	tac	tat	cga	aat	ggc	aaa	gcc	ttt	aag	ttt	ttc	cac	tgg	aat	486
Val	Leu	Tyr	Tyr	Arg	Asn	Gly	Lys	Ala	Phe	Lys	Phe	Phe	His	Trp	Asn	
					140				145					150		
tct	aac	ctc	acc	att	ctg	aaa	acc	aac	ata	agt	cac	aat	ggc	acc	tac	534
Ser	Asn	Leu	Thr	Ile	Leu	Lys	Thr	Asn	Ile	Ser	His	Asn	Gly	Thr	Tyr	
				155					160					165		
cat	tgc	tca	ggc	atg	gga	aag	cat	cgc	tac	aca	tca	gca	gga	ata	tct	582
His	Cys	Ser	Gly	Met	Gly	Lys	His	Arg	Tyr	Thr	Ser	Ala	Gly	Ile	Ser	
			170					175					180			
gtc	act	gtg	aaa	gag	cta	ttt	cca	gct	cca	gtg	ctg	aat	gca	tct	gtg	630
Val	Thr	Val	Lys	Glu	Leu	Phe	Pro	Ala	Pro	Val	Leu	Asn	Ala	Ser	Val	
			185				190					195				
aca	tcc	cca	ctc	ctg	gag	ggg	aat	ctg	gtc	acc	ctg	agc	tgt	gaa	aca	678
Thr	Ser	Pro	Leu	Leu	Glu	Gly	Asn	Leu	Val	Thr	Thr	Ser	Cys	Glu	Thr	
		200				205					210					
aag	ttg	ctc	ttg	cag	agg	cct	ggc	ttg	cag	ctt	tac	ttc	tcc	ttc	tac	726
Lys	Leu	Leu	Leu	Gln	Arg	Pro	Gly	Leu	Gln	Leu	Tyr	Phe	Ser	Phe	Tyr	
		215			220					225				230		
atg	ggc	agc	aag	acc	ctg	cga	ggc	agg	aac	aca	tcc	tct	gaa	tac	caa	774
Met	Gly	Ser	Lys	Thr	Leu	Arg	Gly	Arg	Asn	Thr	Ser	Ser	Glu	Tyr	Gln	
			235					240						245		
ata	cta	act	gct	aga	aga	gaa	gac	tct	ggg	tta	tac	tgg	tgc	gag	gct	822
Ile	Leu	Thr	Ala	Arg	Arg	Glu	Asp	Ser	Gly	Leu	Tyr	Trp	Cys	Glu	Ala	
			250					255					260			
gcc	aca	gag	gat	gga	aat	gtc	ctt	aag	cgc	agc	cct	gag	ttg	gag	ctt	870
Ala	Thr	Glu	Asp	Gly	Asn	Val	Leu	Lys	Arg	Ser	Pro	Glu	Leu	Glu	Leu	
		265					270					275				
caa	gtg	ctt	ggc	ctc	cag	tta	cca	act	cct	gtc	tgg	ttt	cat	gtc	ctt	918
Gln	Val	Leu	Gly	Leu	Gln	Leu	Pro	Thr	Pro	Val	Trp	Phe	His	Val	Leu	
		280				285					290					

11-88L.ST25.txt

ttc tat ctg gca gtg gga ata atg ttt tta gtg aac act gtt ctc tgg	966
Phe Tyr Leu Ala Val Gly Ile Met Phe Leu Val Asn Thr Val Leu Trp	
295 300 305 310	
gtg aca ata cgt aaa gaa ctg aaa aga aag aaa aag tgg gat tta gaa	1014
Val Thr Ile Arg Lys Glu Leu Lys Arg Lys Lys Lys Trp Asp Leu Glu	
315 320 325	
atc tct ttg gat tct ggt cat gag aag aag gta act tcc agc ctt caa	1062
Ile Ser Leu Asp Ser Gly His Glu Lys Lys Val Thr Ser Ser Leu Gln	
330 335 340	
gaa gac aga cat tta gaa gaa gag ctg aaa tgt cag gaa caa aaa gaa	1110
Glu Asp Arg His Leu Glu Glu Glu Leu Lys Cys Gln Glu Gln Lys Glu	
345 350 355	
gaa cag ctg cag gaa ggg gtg cac cgg aag gag ccc cag ggg gcc acg	1158
Glu Gln Leu Gln Glu Gly Val His Arg Lys Glu Pro Gln Gly Ala Thr	
360 365 370	
tagcagcggc tcagtggggtg gccatcgcgc tggaccgtcc cctgccccact tgctcccgct	1218
gagcactgcg tacaaacatc caaaagttca acaacaccag aactgtgtgt ctcctggtat	1278
gtaactctta aagcaataa atgaactgac ttcaaaaaaa aaa	1321

<210> 23
 <211> 374
 <212> PRT
 <213> Homo sapiens

<400> 23

Met Trp Phe Leu Thr Thr Leu Leu Leu Trp Val Pro Val Asp Gly Gln	
1 5 10 15	
Val Asp Thr Thr Lys Ala Val Ile Ser Leu Gln Pro Pro Trp Val Ser	
20 25 30	
Val Phe Gln Glu Glu Thr Val Thr Leu His Cys Glu Val Leu His Leu	
35 40 45	
Pro Gly Ser Ser Ser Thr Gln Trp Phe Leu Asn Gly Thr Ala Thr Gln	
50 55 60	
Thr Ser Thr Pro Ser Tyr Arg Ile Thr Ser Ala Ser Val Asn Asp Ser	
65 70 75 80	
Gly Glu Tyr Arg Cys Gln Arg Gly Leu Ser Gly Arg Ser Asp Pro Ile	
85 90 95	
Gln Leu Glu Ile His Arg Gly Trp Leu Leu Leu Gln Val Ser Ser Arg	
100 105 110	
Val Phe Thr Glu Gly Glu Pro Leu Ala Leu Arg Cys His Ala Trp Lys	

115

120

125

Asp Lys Leu Val Tyr Asn Val Leu Tyr Tyr Arg Asn Gly Lys Ala Phe
 130 135
 Lys Phe Phe His Trp Asn Ser Asn Leu Thr Ile Leu Lys Thr Asn Ile
 145 150 155 160
 Ser His Asn Gly Thr Tyr His Cys Ser Gly Met Gly Lys His Arg Tyr
 165 170 175
 Thr Ser Ala Gly Ile Ser Val Thr Val Lys Glu Leu Phe Pro Ala Pro
 180 185 190
 Val Leu Asn Ala Ser Val Thr Ser Pro Leu Leu Glu Gly Asn Leu Val
 195 200 205
 Thr Leu Ser Cys Glu Thr Lys Leu Leu Leu Gln Arg Pro Gly Leu Gln
 210 215 220
 Leu Tyr Phe Ser Phe Tyr Met Gly Ser Lys Thr Leu Arg Gly Arg Asn
 225 230 235 240
 Thr Ser Ser Glu Tyr Gln Ile Leu Thr Ala Arg Arg Glu Asp Ser Gly
 245 250 255
 Leu Tyr Trp Cys Glu Ala Ala Thr Glu Asp Gly Asn Val Leu Lys Arg
 260 265 270
 Ser Pro Glu Leu Glu Leu Gln Val Leu Gly Leu Gln Leu Pro Thr Pro
 275 280 285
 Val Trp Phe His Val Leu Phe Tyr Leu Ala Val Gly Ile Met Phe Leu
 290 295 300
 Val Asn Thr Val Leu Trp Val Thr Ile Arg Lys Glu Leu Lys Arg Lys
 305 310 315 320
 Lys Lys Trp Asp Leu Glu Ile Ser Leu Asp Ser Gly His Glu Lys Lys
 325 330 335
 Val Thr Ser Ser Leu Gln Glu Asp Arg His Leu Glu Glu Glu Leu Lys
 340 345 350
 Cys Gln Glu Gln Lys Glu Glu Gln Leu Gln Glu Gly Val His Arg Lys
 355 360 365

Glu Pro Gln Gly Ala Thr
370

<210> 24
<211> 1714
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (156)..(1163)

```

<400> 24
gcggggagct tgcagtgacc aagaggggtgt tgaggctagg aggccacgat aaacaggata      60
cgataaaagt ccttaaccaa gacgcagatg ggaagaagcg ttagagcgag cagcactcac      120
atctcaagaa ccagcctttc aaacagtttc cagag atg gat tat cct act tta      173
                Met Asp Tyr Pro Thr Leu
                1                    5

ctt ttg gct ctt ctt cat gta tac aga gct cta tgt gaa gag gtg ctt      221
Leu Leu Ala Leu Leu His Val Tyr Arg Ala Leu Cys Glu Glu Val Leu
                10                    15                    20

tgg cat aca tca gtt ccc ttt gcc gag aac atg tct cta gaa tgt gtg      269
Trp His Thr Ser Val Pro Phe Ala Glu Asn Met Ser Trp Leu Glu Cys Val
                25                    30                    35

tat cca tca atg ggc atc tta aca cag gtg gag tgg ttc aag atc ggg      317
Tyr Pro Ser Met Gly Ile Leu Thr Gln Val Glu Trp Phe Lys Ile Gly
                40                    45                    50

acc cag cag gat tcc ata gcc att ttc agc cct act cat ggc atg gtc      365
Thr Gln Gln Asp Ser Ile Ala Ile Phe Ser Pro Thr His Gly Met Val
                55                    60                    65

ata agg aag ccc tat gct gag agg gtt tac ttt ttg aat tca acg atg      413
Ile Arg Lys Pro Tyr Ala Glu Arg Val Tyr Phe Leu Asn Ser Thr Met
                75                    80                    85

gct tcc aat aac atg act ctt ttc ttt cgg aat gcc tct gaa gat gat      461
Ala Ser Asn Asn Met Thr Leu Phe Phe Arg Asn Ala Ser Glu Asp Asp
                90                    95                    100

gtt ggc tac tat tcc tgc tct ctt tac act tac cca cag gga act tgg      509
Val Gly Tyr Tyr Ser Cys Ser Leu Tyr Thr Tyr Pro Gln Gly Thr Trp
                105                    110                    115

cag aag gtg ata cag gtg gtt cag tca gat agt ttt gag gca gct gtg      557
Gln Lys Val Ile Gln Val Val Gln Ser Asp Ser Phe Glu Ala Ala Val
                120                    125                    130

cca tca aat agc cac att gtt tcg gaa cct gga aag aat gtc aca ctc      605
Pro Ser Asn Ser His Ile Val Ser Glu Pro Gly Lys Asn Val Thr Leu
                135                    140                    145                    150

act tgt cag cct cag atg acg tgg cct gtg cag gca gtg agg tgg gaa      653
Thr Cys Gln Pro Gln Met Thr Trp Pro Val Gln Ala Val Arg Trp Glu
                155                    160                    165

```

11-88L.ST25.txt

aag atc cag ccc cgt cag atc gac ctc tta act tac tgc aac ttg gtc	701
Lys Ile Gln Pro Arg Gln Ile Asp Leu Thr Tyr Cys Asn Leu Val	
170 175 180	
cat ggc aga aat ttc acc tcc aag ttc cca aga caa ata gtg agc aac	749
His Gly Arg Asn Phe Thr Ser Lys Phe Pro Arg Gln Ile Val Ser Asn	
185 190 195	
tgc agc cac gga agg tgg agc gtc atc gtc atc ccc gat gtc aca gtc	797
Cys Ser His Gly Arg Trp Ser Val Ile Val Ile Pro Asp Val Thr Val	
200 205 210	
tca gac tcg ggg ctt tac cgc tgc tac ttg cag gcc agc gca gga gaa	845
Ser Asp Ser Gly Leu Tyr Arg Cys Tyr Leu Gln Ala Ser Ala Gly Glu	
215 220 225 230	
aac gaa acc ttc gtg atg aga ttg act gta gcc gag ggt aaa acc gat	893
Asn Glu Thr Phe Val Met Arg Leu Thr Val Ala Glu Gly Lys Thr Asp	
235 240 245	
aac caa tat acc ctc ttt gtg gct gga ggg aca gtt tta ttg ttg ttg	941
Asn Gln Tyr Thr Leu Phe Val Ala Gly Gly Thr Val Leu Leu Leu	
250 255 260	
ttt gtt atc tca att acc acc atc att gtc att ttc ctt aac aga agg	989
Phe Val Ile Ser Ile Thr Thr Ile Ile Val Ile Phe Leu Asn Arg Arg	
265 270 275	
aga agg aga gag aga aga gat cta ttt aca gag tcc tgg gat aca cag	1037
Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr Glu Ser Trp Asp Thr Gln	
280 285 290	
aag gca ccc aat aac tat aga agt ccc atc tct acc ggt caa cct acc	1085
Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile Ser Thr Gly Gln Pro Thr	
295 300 305 310	
aat caa tcc atg gat gat aca aga gag gat att tat gtc aac tat cca	1133
Asn Gln Ser Met Asp Asp Thr Arg Glu Asp Ile Tyr Val Asn Tyr Pro	
315 320 325	
acc ttc tct cgc aga cca aag act aga gtt taagcttatt cttgacatga	1183
Thr Phe Ser Arg Arg Pro Lys Thr Arg Val	
330 335	
gtgcattagt aatgactctt atgtactcat gcatggatct ttatgcaatt tttttccact	1243
acccaaggtc taccttagat actagtgtgc tgaattgagt tactttgata ggaaaaatac	1303
ttcattacct aaaatcattt ttcatagaac tgtttcagaa aacctgactc taactggttt	1363
atatacaaaa gaaaacttac tgatcatat aacagaaatga tccaggggag attaagcttt	1423
gggcaagggc tatttaccag ggcttaaatg ttgtgtctag aattaagtat gggcataaac	1483
tggtctctga atcccccttc agagtgttg atccatttcc ctggtcttgg cctcactctc	1543
atgcaggctt tcctcttctg ttggcaagat ggctgccaac tcttggaat tcatacatcc	1603
ttgtttctgt ctggtagaga gtttgcttct caaatggagc aaacaaattt gattattttt	1663
tcattgttaa ataggcaaca tgaccataaa ggaatggaatg gcttaagtaa a	1714

11-88L.ST25.txt

<210> 25
 <211> 336
 <212> PRT
 <213> Homo sapiens

<400> 25

Met Asp Tyr Pro Thr Leu Leu Leu Ala Leu Leu His Val Tyr Arg Ala
 1 5 10 15

Leu Cys Glu Glu Val Leu Trp His Thr Ser Val Pro Phe Ala Glu Asn
 20 25 30

Met Ser Leu Glu Cys Val Tyr Pro Ser Met Gly Ile Leu Thr Gln Val
 35 40 45

Glu Trp Phe Lys Ile Gly Thr Gln Gln Asp Ser Ile Ala Ile Phe Ser
 50 55 60

Pro Thr His Gly Met Val Ile Arg Lys Pro Tyr Ala Glu Arg Val Tyr
 65 70 75 80

Phe Leu Asn Ser Thr Met Ala Ser Asn Asn Met Thr Leu Phe Phe Arg
 85 90 95

Asn Ala Ser Glu Asp Asp Val Gly Tyr Tyr Ser Cys Ser Leu Tyr Thr
 100 105 110

Tyr Pro Gln Gly Thr Trp Gln Lys Val Ile Gln Val Val Gln Ser Asp
 115 120 125

Ser Phe Glu Ala Ala Val Pro Ser Asn Ser His Ile Val Ser Glu Pro
 130 135 140

Gly Lys Asn Val Thr Leu Thr Cys Gln Pro Gln Met Thr Trp Pro Val
 145 150 155 160

Gln Ala Val Arg Trp Glu Lys Ile Gln Pro Arg Gln Ile Asp Leu Leu
 165 170 175

Thr Tyr Cys Asn Leu Val His Gly Arg Asn Phe Thr Ser Lys Phe Pro
 180 185 190

Arg Gln Ile Val Ser Asn Cys Ser His Gly Arg Trp Ser Val Ile Val
 195 200 205

Ile Pro Asp Val Thr Val Ser Asp Ser Gly Leu Tyr Arg Cys Tyr Leu
 210 215 220

11-88L.ST25.txt

Gln Ala Ser Ala Gly Glu Asn Glu Thr Phe Val Met Arg Leu Thr Val
 225 230 235 240

Ala Glu Gly Lys Thr Asp Asn Gln Tyr Thr Leu Phe Val Ala Gly Gly
 245 250 255

Thr Val Leu Leu Leu Leu Phe Val Ile Ser Ile Thr Thr Ile Ile Val
 260 265 270

Ile Phe Leu Asn Arg Arg Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr
 275 280 285

Glu Ser Trp Asp Thr Gln Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile
 290 295 300

Ser Thr Gly Gln Pro Thr Asn Gln Ser Met Asp Asp Thr Arg Glu Asp
 305 310 315 320

Ile Tyr Val Asn Tyr Pro Thr Phe Ser Arg Arg Pro Lys Thr Arg Val
 325 330 335

<210> 26
 <211> 2107
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (35)..(1975)

<400> 26
 acgcggaac aggccttgac ccagacacga cacc atg cat ctc ctc ggc ccc tgg 55
 Met His Leu Leu Gly Pro Trp
 1 5
 ctc ctg ctc ctg gtt cta gaa tac ttg gct ttc tct gac tca agt aaa 103
 Leu Leu Leu Leu Val Leu Glu Tyr Leu Ala Phe Ser Asp Ser Ser Lys
 10 15 20
 tgg gtt ttt gag cac cct gaa acc ctc tac gcc tgg gag ggg gcc tgc 151
 Trp Val Phe Glu His Pro Glu Thr Leu Tyr Ala Trp Glu Gly Ala Cys
 25 30 35
 gtc tgg atc ccc tgc acc tac aga gcc cta gat ggt gac ctg gaa agc 199
 Val Trp Ile Pro Cys Thr Tyr Arg Ala Leu Asp Gly Asp Leu Glu Ser
 40 45 50 55
 ttc atc ctg ttc cac aat cct gag tat aac aag aac acc tgc aag ttt 247
 Phe Ile Leu Phe His Asn Pro Glu Tyr Asn Lys Asn Thr Ser Lys Phe
 60 65 70
 gat ggg aca aga ctc tat gaa agc aca aag gat ggg aag gtt cct tct 295
 Asp Gly Thr Arg Leu Tyr Glu Ser Thr Lys Asp Gly Lys Val Pro Ser
 75 80 85

11-88L.ST25.txt

gag Glu	cag Gln	aaa Lys 90	agg Arg	gtg Val	caa Gln	ttc Phe	ctg Leu 95	gga Gly	gac Asp	aag Lys	aat Asn	aag Lys 100	aac Asn	tgc Cys	aca Thr	343
ctg Leu	agt Ser 105	atc Ile	cac His	ccg Pro	gtg Val	cac His 110	ctc Leu	aat Asn	gac Asp	agt Ser	ggt Gly 115	cag Gln	ctg Leu	ggg Gly	ctg Leu	391
agg Arg 120	atg Met	gag Glu	tcc Ser	aag Lys	act Thr 125	gag Glu	aaa Lys	tgg Trp	atg Met	gaa Glu 130	cga Arg	ata Ile	cac His	ctc Leu	aat Asn 135	439
gtc Val	tct Ser	gaa Glu	agg Arg	cct Pro 140	ttt Phe	cca Pro	cct Pro	cat His	atc Ile 145	cag Gln	ctc Leu	cct Pro	cca Pro	gaa Glu 150	att Ile	487
caa Gln	gag Glu	tcc Ser 155	cag Gln	gaa Glu	gtc Val	act Thr	ctg Leu	acc Thr 160	tgc Cys	ttg Leu	ctg Leu	aat Asn	ttc Phe 165	tcc Ser	tgc Cys	535
tat Tyr	ggg Gly	tat Tyr 170	ccg Pro	atc Ile	caa Gln	ttg Leu	cag Gln 175	tgg Trp	ctc Leu	cta Leu	gag Glu	ggg Gly 180	ggt Val	cca Pro	atg Met	583
agg Arg 185	cag Gln	gct Ala	gct Ala	gtc Val	acc Thr	tgc Ser 190	tcc Thr	ttg Ser	acc Leu	atc Thr 195	aag Lys	tct Ser	gtc Val	ttc Phe		631
acc Thr 200	cgg Arg	agc Ser	gag Glu	ctc Leu	aag Lys 205	ttc Phe	tcc Ser	cca Pro	cag Gln	tgg Trp 210	agt Ser	cac His	cat His	ggg Gly 215	aag Lys 215	679
att Ile	gtg Val	acc Thr	tgc Cys	cag Gln 220	ctt Leu	cag Gln	gat Asp	gca Ala	gat Asp 225	ggg Gly	aag Lys	ttc Phe	ctc Leu	tcc Ser 230	aat Asn	727
gac Asp	acg Thr	gtg Val	cag Gln	ctg Leu	aac Asn	gtg Val	aag Lys	cat His 240	cct Pro	ccc Pro	aag Lys	aag Lys	gtg Val 245	acc Thr	aca Thr	775
gtg Val	att Ile	caa Gln 250	aac Asn	ccc Pro	atg Met	ccg Pro	att Ile 255	cga Arg	gaa Glu	gga Gly	gac Asp	aca Thr 260	gtg Val	acc Thr	ctt Leu	823
tcc Ser	tgt Cys 265	aac Asn	tac Tyr	aat Asn	tcc Ser	agt Ser 270	aac Asn	ccc Pro	agt Ser	gtt Val	acc Thr 275	cgg Arg	tat Tyr	gaa Glu	tgg Trp	871
aaa Lys 280	ccc Pro	cat His	ggc Gly	gcc Ala	tgg Trp 285	gag Glu	gag Glu	cca Pro	tgc Ser	ctt Leu 290	ggg Gly	gtg Val	ctg Leu	aag Lys 295	atc Ile 295	919
caa Gln	aac Asn	gtt Val	ggc Gly	tgg Trp 300	gac Asp	aac Asn	aca Thr	acc Thr	atc Ile 305	gcc Ala	tgc Cys	gca Ala	gct Ala	tgt Cys 310	aat Asn	967
agt Ser	tgg Trp	tgc Cys	tgc Trp 315	tgg Trp	gcc Ala	tcc Ser	cct Pro	gtc Val 320	gcc Ala	ctg Leu	aat Asn	gtc Val	cag Gln 325	tat Tyr	gcc Ala	1015
ccc Pro	cga Arg	gac Asp 330	gtg Val	agg Arg	gtc Val	cgg Arg	aaa Lys 335	atc Ile	aag Lys	ccc Pro	ctt Leu	tcc Ser 340	gag Glu	att Ile	cac His	1063

11-88L.ST25.txt

tct gga aac tcg gtc agc ctc caa tgt gac ttc tca agc agc cac ccc Ser Gly Asn Ser Val Ser Leu Gln Cys Asp Phe Ser Ser His Pro	1111
345	
aaa gaa gtc cag ttc ttc tgg gag ggc agg ctt ctg ggg aaa Lys Glu Val Gln Phe Phe Trp Glu Lys Asn Gly Arg Leu Leu Gly Lys	1159
360 365 370 375	
gaa agc cag ctg aat ttt gac tcc atc tcc cca gaa gat gct ggg agt Glu Ser Gln Leu Asn Phe Asp Ser Ile Ser Pro Glu Asp Ala Gly Ser	1207
380 385 390	
tac agc tgc tgg gtg aac aac tcc ata gga cag aca gcg tcc aag gcc Tyr Ser Cys Trp Val Asn Asn Ser Ile Gly Gln Thr Ala Ser Lys Ala	1255
395 400	
tgg aca ctt gaa gtg ctg tat gca ccc agg agg ctg cgt gtg tcc atg Trp Thr Leu Glu Val Leu Tyr Ala Pro Arg Arg Leu Val Ser Met	1303
410 415	
agc ccg ggg gac caa gtg atg gag ggg aag agt gca acc ctg acc tgt Ser Pro Gly Asp Gln Val Met Glu Gly Lys Ser Ala Thr Leu Thr Cys	1351
425 430 435	
gag agc gac gcc aac cct ccc gtc tcc cac tac acc tgg ttt gac tgg Glu Ser Asp Ala Asn Pro Pro Val Ser His Tyr Thr Trp Phe Asp Trp	1399
440 445 450 455	
aat aac caa agc ctc ccc tac cac agc cag aag ctg aga ttg gag ccg Asn Asn Gln Ser Leu Pro Tyr His Ser Gln Lys Leu Arg Leu Glu Pro	1447
460 465 470	
gtg aag gtc cag cac tcg ggt gcc tac tgg tgc cag ggg acc aac agt Val Lys Val Gln His Ser Gly Ala Tyr Trp Cys Gln Gly Thr Asn Ser	1495
475 480	
gtg ggc aag ggc cgt tcg cct ctc agc acc ctc acc gtc tac tat agc Val Gly Lys Gly Arg Ser Pro Leu Ser Thr Leu Thr Val Tyr Tyr Ser	1543
490 495 500	
ccg gag acc atc ggc agg cga gtg gct gtg gga ctc ggg tcc tgc ctc Pro Glu Thr Ile Gly Arg Val Ala Val Gly Leu Gly Ser Cys Leu	1591
505 510 515	
gcc atc ctc atc ctg gca atc tgt ggg ctc aag ctc cag cga cgt tgg Ala Ile Leu Ile Leu Ala Ile Cys Gly Leu Lys Leu Gln Arg Arg Trp	1639
520 525 530 535	
aag agg aca cag agc cag cag ggg ctt cag gag aat tcc agc ggc cag Lys Arg Thr Gln Ser Gln Gln Gly Leu Gln Glu Asn Ser Ser Gly Gln	1687
540 545 550	
agc ttc ttt gtg agg aat aaa aag gtt aga agg gcc ccc ctc tct gaa Ser Phe Phe Val Arg Asn Lys Lys val Arg Arg Ala Pro Leu Ser Glu	1735
555 560 565	
ggc ccc cac tcc ctg gga tgc tac aat cca atg atg gaa gat ggc att Gly Pro His Ser Leu Gly Cys Tyr Asn Pro Met Met Glu Asp Gly Ile	1783
570 575 580	
agc tac acc acc ctg cgc ttt ccc gag atg aac ata cca cga act gga Ser Tyr Thr Thr Leu Arg Phe Pro Glu Met Asn Ile Pro Arg Thr Gly	1831

[illegible]

11-88L.S125.txt

Ile Gln Leu Pro Pro Glu Ile Gln Glu Ser Gln Glu Val Thr Leu Thr
145 150 155 160

Cys Leu Leu Asn Phe Ser Cys Tyr Gly Tyr Pro Ile Gln Leu Gln Trp
165 170 175

Leu Leu Glu Gly Val Pro Met Arg Gln Ala Ala Val Thr Ser Thr Ser
180 185 190

Leu Thr Ile Lys Ser Val Phe Thr Arg Ser Glu Leu Lys Phe Ser Pro
195 200 205

Gln Trp Ser His His Gly Lys Ile Val Thr Cys Gln Leu Gln Asp Ala
210 215 220

Asp Gly Lys Phe Leu Ser Asn Asp Thr Val Gln Leu Asn Val Lys His
225 230 235 240

Pro Pro Lys Lys Val Thr Thr Val Ile Gln Asn Pro Met Pro Ile Arg
245 250 255

Glu Gly Asp Thr Val Thr Leu Ser Cys Asn Tyr Asn Ser Ser Asn Pro
260 265 270

Ser Val Thr Arg Tyr Glu Trp Lys Pro His Gly Ala Trp Glu Glu Pro
275 280 285

Ser Leu Gly Val Leu Lys Ile Gln Asn Val Gly Trp Asp Asn Thr Thr
290 295 300

Ile Ala Cys Ala Ala Cys Asn Ser Trp Cys Ser Trp Ala Ser Pro Val
305 310 315 320

Ala Leu Asn Val Gln Tyr Ala Pro Arg Asp Val Arg Val Arg Lys Ile
325 330 335

Lys Pro Leu Ser Glu Ile His Ser Gly Asn Ser Val Ser Leu Gln Cys
340 345 350

Asp Phe Ser Ser Ser His Pro Lys Glu Val Gln Phe Phe Trp Glu Lys
355 360 365

Asn Gly Arg Leu Leu Gly Lys Glu Ser Gln Leu Asn Phe Asp Ser Ile
370 375 380

Ser Pro Glu Asp Ala Gly Ser Tyr Ser Cys Trp Val Asn Asn Ser Ile
385 390 395 400

Gly Gln Thr Ala Ser Lys Ala Trp Thr Leu Glu Val Leu Tyr Ala Pro
 405 410 415
 Arg Arg Leu Arg Val Ser Met Ser Pro Gly Asp Gln Val Met Glu Gly
 420 425 430
 Lys Ser Ala Thr Leu Thr Cys Glu Ser Asp Ala Asn Pro Pro Val Ser
 435 440 445
 His Tyr Thr Trp Phe Asp Trp Asn Asn Gln Ser Leu Pro Tyr His Ser
 450 455 460
 Gln Lys Leu Arg Leu Glu Pro Val Lys Val Gln His Ser Gly Ala Tyr
 465 470 475 480
 Trp Cys Gln Gly Thr Asn Ser Val Gly Lys Gly Arg Ser Pro Leu Ser
 485 490 495
 Thr Leu Thr Val Tyr Tyr Ser Pro Glu Thr Ile Gly Arg Arg Val Ala
 500 505 510
 Val Gly Leu Gly Ser Cys Leu Ala Ile Leu Ile Leu Ala Ile Cys Gly
 515 520 525
 Leu Lys Leu Gln Arg Arg Trp Lys Arg Thr Gln Ser Gln Gln Gly Leu
 530 535 540
 Gln Glu Asn Ser Ser Gly Gln Ser Phe Phe Val Arg Asn Lys Lys Val
 545 550 555 560
 Arg Arg Ala Pro Leu Ser Glu Gly Pro His Ser Leu Gly Cys Tyr Asn
 565 570 575
 Pro Met Met Glu Asp Gly Ile Ser Tyr Thr Thr Leu Arg Phe Pro Glu
 580 585 590
 Met Asn Ile Pro Arg Thr Gly Asp Ala Glu Ser Ser Glu Met Gln Arg
 595 600 605
 Pro Pro Pro Asp Cys Asp Asp Thr Val Thr Tyr Ser Ala Leu His Lys
 610 615 620
 Arg Gln Val Gly Thr Met Arg Thr Ser Phe Gln Ile Phe Gln Lys Met
 625 630 635 640
 Arg Gly Phe Ile Thr Gln Ser

<210> 28
 <211> 1200
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (101)..(880)

<400> 28
 ggggtgcaaa gaagagacag cagcgcccag cttggagggtg ctaactccag aggccagcat 60
 cagcaactgg gcacagaaag gagccgcctg ggcaggggacc atg gca cgg cca cat 115
 1 Met Ala Arg Pro His 5
 ccc tgg tgg ctg tgc gtt ctg ggg acc ctg gtg ggg ctc tca gct act 163
 Pro Trp Trp Leu Cys Val Leu Gly Thr Leu Val Gly Leu Ser Ala Thr 20
 10
 cca gcc ccc aag agc tgc cca gag agg cac tac tgg gct cag gga aag 211
 Pro Ala Pro Lys Ser Cys Pro Glu Arg His Tyr Trp Ala Gln Gly Lys 35
 25
 ctg tgc tgc cag atg tgt gag cca gga aca ttc ctc gtg aag gac tgt 259
 Leu Cys Cys Gln Met Cys Glu Pro Gly Thr Phe Leu Val Lys Asp Cys 45
 40
 gac cag cat aga aag gct gct cag tgt gat cct tgc ata ccg ggg gtc 307
 Asp Gln His Arg Lys Ala Ala Gln Cys Asp Pro Cys Ile Pro Gly Val 60
 55
 tcc ttc tct cct gac cac cac acc cgg ccc cac tgt gag agc tgt cgg 355
 Ser Phe Ser Pro Asp His His Thr Arg Pro His Cys Glu Ser Cys Arg 75
 70
 cac tgt aac tct ggt ctt ctc gtt cgc aac tgc acc atc act gcc aat 403
 His Cys Asn Ser Gly Leu Leu Val Arg Asn Cys Thr Ile Thr Ala Asn 90
 95
 gct gag tgt gcc tgt cgc aat ggc tgg cag tgc agg gac aag gag tgc 451
 Ala Glu Cys Ala Cys Arg Asn Gly Trp Gln Cys Arg Asp Lys Glu Cys 105
 110
 acc gag tgt gat cct ctt cca aac cct tcg ctg acc gct cgg tcg tct 499
 Thr Glu Cys Asp Pro Leu Pro Asn Pro Ser Leu Thr Ala Arg Ser Ser 125
 120
 cag gcc ctg agc cca cac cct cag ccc acc cac tta cct tat gtc agt 547
 Gln Ala Leu Ser Pro His Pro Gln Pro Thr His Leu Pro Tyr Val Ser 135
 140
 gag atg ctg gag gcc agg aca gct ggg cac atg cag act ctg gct gac 595
 Glu Met Leu Glu Ala Arg Thr Ala Gly His Met Leu Gln Thr Leu Ala Asp 155
 160
 ttc agg cag ctg cct gcc cgg act ctc tct acc cac tgg cca ccc caa 643
 Phe Arg Gln Leu Pro Ala Arg Thr Leu Ser Thr His Trp Pro Pro Gln 175
 180

11-86L.ST25.txt

```

aga tcc ctg tgc agc tcc gat ttt att cgc atc ctt gtg atc ttc tct      691
Arg Ser Leu Cys Ser Ser Asp Phe Ile Arg Ile Leu Val Ile Phe Ser
185                               190                               195

gga atg ttc ctt gtt ttc acc ctg gcc ggg gcc ctg ttc ctc cat caa      739
Gly Met Phe Leu Val Phe Thr Leu Ala Gly Ala Leu Phe Leu His Gln
200                               205                               210

cga agg aaa tat aga tca aac aaa gga gaa agt cct gtg gag cct gca      787
Arg Arg Lys Tyr Arg Ser Asn Lys Gly Glu Ser Pro Val Glu Pro Ala
215                               220                               225

gag cct tgt cgt tac agc tgc ccc agg gag gag gag ggc agc acc atc      835
Glu Pro Cys Arg Tyr Ser Cys Pro Arg Glu Glu Glu Glu Gly Ser Thr Ile
230                               235                               240                               245

ccc atc cag gag gat tac cga aaa ccg gag cct gcc tgc tcc ccc      880
Pro Ile Gln Glu Asp Tyr Arg Lys Pro Glu Pro Ala Cys Ser Pro
250                               255                               260

tgagccagca cctgcggtag ctgcactaca gccctggcct ccacccccac ccgcccagcc      940
atccaagggga gaggagagacc tggcagccac aactgcagtc ccatcctctt gtcagggccc      1000
tttctgtgt acacgtgaca gaggccttt tcgagactgg cagggagcag gacaaatatg      1060
gatgaggtgg agagtgggaa gcaggagccc agccagctgc gcgcgcgtgc agggggcg      1120
gggctctggt tgtaaggcac acttctctgt gcgaaagacc cacatgctac aagacgggca      1180
aaataaagtg acagatgacc      1200

<210> 29
<211> 260
<212> PRT
<213> Homo sapiens

<400> 29
Met Ala Arg Pro His Pro Trp Trp Leu Cys Val Leu Gly Thr Leu Val
1 5 10 15

Gly Leu Ser Ala Thr Pro Ala Pro Lys Ser Cys Pro Glu Arg His Tyr
20 25 30

Trp Ala Gln Gly Lys Leu Cys Cys Gln Met Cys Glu Pro Gly Thr Phe
35 40 45

Leu Val Lys Asp Cys Asp Gln His Arg Lys Ala Ala Gln Cys Asp Pro
50 55 60

Cys Ile Pro Gly Val Ser Phe Ser Pro Asp His His Thr Arg Pro His
65 70 75 80

Cys Glu Ser Cys Arg His Cys Asn Ser Gly Leu Leu Val Arg Asn Cys
85 90 95

```

11-88L.ST25.txt

Thr Ile Thr Ala Asn Ala Glu Cys Ala Cys Arg Asn Gly Trp Gln Cys
100 105 110

Arg Asp Lys Glu Cys Thr Glu Cys Asp Pro Leu Pro Asn Pro Ser Leu
115 120 125

Thr Ala Arg Ser Ser Gln Ala Leu Ser Pro His Pro Gln Pro Thr His
130 135 140

Leu Pro Tyr Val Ser Glu Met Leu Glu Ala Arg Thr Ala Gly His Met
145 150 155 160

Gln Thr Leu Ala Asp Phe Arg Gln Leu Pro Ala Arg Thr Leu Ser Thr
165 170 175

His Trp Pro Pro Gln Arg Ser Leu Cys Ser Ser Asp Phe Ile Arg Ile
180 185 190

Leu Val Ile Phe Ser Gly Met Phe Leu Val Phe Thr Leu Ala Gly Ala
195 200 205

Leu Phe Leu His Gln Arg Arg Lys Tyr Arg Ser Asn Lys Gly Glu Ser
210 215 220

Pro Val Glu Pro Ala Glu Pro Cys Arg Tyr Ser Cys Pro Arg Glu Glu
225 230 235 240

Glu Gly Ser Thr Ile Pro Ile Gln Glu Asp Tyr Arg Lys Pro Glu Pro
245 250 255

Ala Cys Ser Pro
260

<210> 30
<211> 2350
<212> DNA
<213> Homo sapiens

<400> 30
ctccctttgg gcaaggacct gagacccttg tgctaagtca agaggctcaa tgggctgcag 60
aagaactaga gaaggaccaa gcaaagccat gatatttcca tggaaatgtc agagcaccca 120
gagggactta tggaaactct tcaagttgtg ggggtggaca atgctctgtt gtgatttctt 180
ggcacatcat ggaaccgact gctggactta ccattattct gaaaaaccca tgaactggca 240
aagggtctaga agattctgcc gagacaatta cacagattta gttgccatag aaacaaggc 300
ggaaattgag tatctggaga agactctgcc ttctagtcgt tcttactact ggataggaat 360

11-88L.ST25.txt

ccggaagata	ggaggaatat	ggacgtgggt	gggaaccaac	aaatctctca	ctgaagaagc	420
agagaactgg	ggagatgggt	agcccaacaa	caagaagaac	aaggaggact	gcgtggagat	480
ctatatcaag	agaacaaga	atgcaggcaa	atggaacgat	gacgcctgcc	acaaactaaa	540
ggcagccctc	tgttacacag	cttcttgcca	gccctgggtc	tgcagtggcc	atggagaatg	600
tgtagaaatc	atcaataatt	acacctgcaa	ctgtgatgtg	gggtactatg	ggccccagtg	660
tcagtttggt	attcagtggt	agcctttgga	ggccccagag	ctgggtacca	tggactgtac	720
tcactctttg	ggaaacttca	gcttcagctc	acagtgtgcc	ttcagctgct	ctgaaggaac	780
aaacttaact	gggattgaag	aaaccacctg	tggaccattt	ggaaactggt	catctccaga	840
accaacctgt	caagtgttc	agtgtgagcc	tctatcagca	ccagatttgg	ggatcatgaa	900
ctgtagccat	cccttgccca	gcttcagctt	tacctctgca	tgtaccttca	tctgctcaga	960
aggaactgag	ttaattggga	agaagaaaac	catttgtgaa	tcacttgga	tctgggtcaa	1020
tcctagtcca	atatgtcaaa	aattggacaa	aagtcttcca	atgattaaag	agggtgatta	1080
taacccccct	ttcattccag	tggcagtcac	ggttactgca	ttctctgggt	tggcatttat	1140
catttggtg	gcaaggagat	taaaaaaagg	caagaaatcc	aagagaagta	tgaatgacct	1200
atattaaatc	gcccttggtg	aaagaaaatt	cttggaatac	taaaaatcat	gagatccttt	1260
aaatccttcc	atgaacggtt	ttgtgtggtg	gcacctccta	cgtcaaacat	gaagtgtggt	1320
tccttcagtg	catctgggaa	gatttctacc	tgaccaacag	ttccttcagc	ttccatttcg	1380
ccccctcatt	atccctcaac	ccccagccca	caggtgttta	tacagctcag	ctttttgtct	1440
tttctgagga	gaaacaaata	agaccataaa	gggaaaggat	tcattgtgga	tataaagatg	1500
gctgactttg	ctctttcttg	actcttggtt	tcagtttcaa	ttcagtgtct	tacttgatga	1560
cagacacttc	taaatgaagt	gcaaatgtga	tacatatgtg	aatatggact	cagttttctt	1620
gcagatcaaa	tttcacgtcg	tcttctgtat	actgtggagg	tacactctta	tagaaagtgc	1680
aaaaagtcta	cgtctctctt	tctttctaac	tccagtgaag	taattgggtc	ctgctcaagt	1740
tgaagagatc	ctatttgcac	tgtagcctcg	ccgtctgtga	attggaccat	cctattttaac	1800
tggcttcagc	ctccccacct	tcttcagcca	ctctctcttt	tcagttggct	gacttcacac	1860
cctagcatct	catgagtgcc	aagcaaaagg	agagaagaga	gaaatagcct	gcgctgtttt	1920
ttagtttggg	ggttttgcgt	tttcttttta	tgagaccat	tcctatttct	tatagtcaat	1980
gtttctttta	tcagatatt	attagtaaga	aaacatcact	gaaatgctag	ctgcaagtga	2040
catctctttg	atgtcatatg	gaagagttaa	aacaggtgga	gaaattcctt	gattcacaat	2100
gaaatgtctc	cttttccctc	gccccagac	cttttatccg	acttacctag	attctacata	2160
ttctttaaat	ttcatctcag	gcctccctca	acccaccac	ttcttttata	actagtcctt	2220

11-88L.ST25.txt

tactaatcca acccatgatg agctcctctt cctggcttct tactgaaagg ttaccctgta 2280
 acatgcaatt ttgcatttga ataaagcctg ctttttaagt gttaaaaaaa aaaaaaaaaa 2340
 aaaaaaaaaa 2350

<210> 31
 <211> 1354
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (116)..(1198)

<400> 31
 ccagcctctg ccagggttcgg tcgcgatcc tcgtcccgtc ctccgccggc ccctgccccg 60
 cgcccaggga tcctccagct cctttcgccc gcgccctcgg ttcgctccgg acacc atg 118
 Met
 1
 gac aag ttt tgg tgg cac gca gcc tgg gga ctc tgc ctc gtg ccg ctg 166
 Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro Leu
 5 10 15
 agc ctg gcg cag atc gat ttg aat ata acc tgc cgc ttt gca ggt gta 214
 Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly Val
 20 25 30
 ttc cac gtg gag aaa aat ggt cgc tac agc atc tct cgc acg gag gcc 262
 Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu Ala
 35 40 45
 gct gac ctc tgc aag gct ttc aat agc acc ttg ccc aca atg gcc cag 310
 Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala Gln
 50 55 60 65
 atg gag aaa gct ctg agc atc gga ttt gag acc tgc agg tat ggg ttc 358
 Met Glu Lys Ala Leu Ser Ile Gly Phe Gly Thr Cys Arg Tyr Phe
 70 75 80
 ata gaa ggg cat gtg gtg att ccc cgg atc cac ccc aac tcc atc tgt 406
 Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile Cys
 85 90 95
 gca gca aac aac aca ggg gtg tac atc ctc aca tac aac acc tcc cag 454
 Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser Gln
 100 105 110
 tat gac aca tat tgc ttc aat gct tca gct cca cct gaa gaa gat tgt 502
 Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp Cys
 115 120 125
 aca tca gtc aca gac ctg ccc aat gcc ttt gat gga cca att acc ata 550
 Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr Ile
 130 135 140 145
 act att gtt aac cgt gat ggc acc cgc tat gtc cag aaa gga gaa tac 598
 Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu Tyr
 150 155 160

11-88L.ST25.txt

```

aga acg aat cct gaa gac atc tac ccc agc aac cct act gat gat gac   646
Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp Asp
165 170 175

gtg agc agc ggc tcc tcc agt gaa agg agc agc act tca gga ggt tac   694
Val Ser Ser Gly Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly Tyr
180 185 190

atc ttt tac acc ttt tct act gta cac ccc atc cca gac gaa gac agt   742
Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp Ser
195 200 205

ccc tgg atc acc gac agc aca gac aga atc cct gct acc aga gac caa   790
Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Ala Thr Arg Asp Gln
210 215 220 225

gac aca ttc cac ccc agt ggg ggg tcc cat acc act cat gaa tct gaa   838
Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr His Glu Ser Glu
230 235 240

tca gat gga cac tca cat ggg agt caa gaa ggt gga gca aac aca acc   886
Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Ala Asn Thr Thr
245 250 255

tct ggt cct ata agg aca ccc caa att cca gaa tgg ctg atc atc ttg   934
Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp Leu Ile Ile Leu
260 265 270

gca tcc ctc ttg gcc ttg gct ttg att ctt gca gtt tgc att gca gtc   982
Ala Ser Leu Leu Ala Leu Leu Ile Leu Ala Val Val Cys Ile Ala Val
275 280 285

aac agt cga aga agg tgt ggg cag aag aaa aag cta gtg atc aac agt   1030
Asn Ser Arg Arg Arg Cys Gly Gln Lys Lys Lys Leu Val Ile Asn Ser
290 295 300 305

ggc aat gga gct gtg gag gac aga aag cca agt gga ctc aac gga gag   1078
Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser Gly Leu Asn Gly Glu
310 315 320

gcc agc aag tct cag gaa atg gtg cat ttg gtg aac aag gag tcg tca   1126
Ala Ser Lys Ser Gln Glu Met Val His Leu Val Asn Lys Glu Ser Ser
325 330 335

gaa act cca gac cag ttt atg aca gct gat gag aca agg aac ctg cag   1174
Glu Thr Pro Asp Gln Phe Met Thr Ala Asp Glu Thr Arg Asn Leu Gln
340 345 350

aat gtg gac atg aag att ggg gtg taacacctac accattatct tggaagaaaa   1228
Asn Val Asp Met Lys Ile Gly Val
355 360

caaccgttgt aaacataacc attacaggga gctgggacac ttaacagatg caatgtgcta   1288

ctgattgttt cattgcgaat ctttttagc ataaaaatct ctactctttt tgttaaaaaa   1348

aaaaaa   1354

```

```

<210> 32
<211> 361
<212> PRT

```

<213> Homo sapiens

<400> 32

Met Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro
 1 5 10 15

Leu Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly
 20 25 30

Val Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu
 35 40 45

Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala
 50 55 60

Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly
 65 70 75 80

Phe Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile
 85 90 95

Cys Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser
 100 105 110

Gln Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp
 115 120 125

Cys Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr
 130 135 140

Ile Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu
 145 150 155 160

Tyr Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp
 165 170 175

Asp Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly
 180 185 190

Tyr Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp
 195 200 205

Ser Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Ala Thr Arg Asp
 210 215 220

Gln Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr His Glu Ser
 225 230 235 240

11-88L.ST25.txt

Glu Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Gly Ala Asn Thr
 245 250 255
 Thr Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp Leu Ile Ile
 260 265 270
 Leu Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu Ala Val Cys Ile Ala
 275 280 285
 Val Asn Ser Arg Arg Arg Cys Gly Gln Lys Lys Lys Leu Val Ile Asn
 290 295 300
 Ser Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser Gly Leu Asn Gly
 305 310 315 320
 Glu Ala Ser Lys Ser Gln Glu Met Val His Leu Val Asn Lys Glu Ser
 325 330 335
 Ser Glu Thr Pro Asp Gln Phe Met Thr Ala Asp Glu Thr Arg Asn Leu
 340 345 350
 Gln Asn Val Asp Met Lys Ile Gly Val
 355 360

<210> 33
 <211> 2308
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (116)..(1594)

<400> 33
 ccagcctctg ccaggttcgg tccgccatcc tcgtcccgtc ctccgccggc cctcgccccg 60
 cgcccaggga tcttccagct ctttcgccc gcgccttcg ttcgtccgg acacc atg 118
 Met
 1
 gac aag ttt tgg tgg cac gca gcc tgg gga ctc tgc ctc gtg ccg ctg 166
 Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro Leu
 5 10 15
 agc ctg gcg cag atc gat ttg aat ata acc tgc cgc ttt gca ggt gta 214
 Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly Val
 20 25 30
 ttc cac gtg gag aaa aat ggt cgc tac agc atc tct cgg acg gag gcc 262
 Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu Ala
 35 40 45
 gct gac ctc tgc aag gct ttc aat agc acc ttg ccc aca atg gcc cag 310

11-88L.5T25.txt

Ala 50	Asp	Leu	Cys	Lys	Ala 55	Phe	Asn	Ser	Thr	Leu 60	Pro	Thr	Met	Ala	Gln 65	
atg Met	gag Glu	aaa Lys	gct Ala	ctg Leu 70	agc Ser	atc Ile	gga Gly	ttt Phe 75	gag Glu	acc Thr	tgc Cys	agg Arg	tat Tyr	ggg Gly 80	ttc Phe	358
ata Ile	gaa Glu	ggg Gly	cat His 85	gtg Val	gtg Val	att Ile	ccc Pro	cgg Arg 90	atc Ile	cac His	ccc Pro	aac Asn	tcc Ser 95	atc Ile	tgt Cys	406
gca Ala	gca Ala	aac Asn 100	aac Asn	aca Thr	ggg Gly	gtg Val	tac Tyr 105	atc Ile	ctc Leu	aca Thr	tac Tyr	aac Asn 110	acc Thr	tcc Ser	cag Gln	454
tat Tyr	gac Asp 115	aca Thr	tat Tyr	tgc Cys	ttc Phe	aat Asn 120	gct Ala	tca Ser	gct Ala	cca Pro	cct Pro 125	gaa Glu	gaa Glu	gat Asp	tgt Cys	502
aca Thr 130	tca Ser	gtc Val	aca Thr	gac Asp	ctg Leu 135	ccc Pro	aat Asn	gcc Ala	ttt Phe	gat Asp 140	gga Gly	cca Pro	att Ile	acc Thr	ata Ile 145	550
act Thr	att Ile	gtt Val	aac Asn	cgt Arg 150	gat Asp	ggc Gly	acc Thr	cgc Arg	tat Tyr 155	gtc Val	cag Gln	aaa Lys	gga Gly	gaa Glu 160	tac Tyr	598
aga Arg	acg Thr	aat Asn	cct Pro 165	gaa Glu	gac Asp	atc Ile	tac Tyr	ccc Pro 170	agc Ser	aac Asn	cct Pro	act Thr	gat Asp 175	gat Asp	gac Asp	646
gtg Val	agc Ser	agc Ser 180	ggc Gly	tcc Ser	tcc Ser	agt Ser	gaa Glu 185	agg Arg	agc Ser	agc Ser	act Thr	tca Ser 190	gga Gly	ggt Gly	tac Tyr	694
atc Ile 195	ttt Phe	tac Tyr	acc Thr	ttt Phe	tct Ser	act Thr 200	gta Val	cac His	ccc Pro	atc Ile	cca Pro 205	gac Asp	gaa Glu	gac Asp	agt Ser	742
ccc Pro 210	tgg Trp	atc Ile	acc Thr	gac Asp	agc Ser 215	aca Thr	gac Asp	aga Arg	atc Ile	cct Pro 220	cgt Arg	acc Thr	aat Asn	atg Met	gac Asp 225	790
tcc Ser	agt Ser	cat His	agt Ser	aca Thr 230	acg Thr	ctt Leu	cag Gln	cct Pro	act Pro 235	gca Ala	aat Asn	cca Pro	aac Asn	aca Thr 240	ggg Gly	838
ttg Leu	gtg Val	gaa Glu	gat Asp 245	ttg Leu	gac Asp	agg Arg	aca Thr	gga Gly 250	cct Pro	ctt Leu	tca Ser	atg Met	aca Thr 255	acg Thr	cag Gln	886
cag Gln	agt Ser	aat Asn 260	tct Ser	cag Gln	agc Ser	ttc Phe	tct Ser 265	aca Thr	tca Ser	cat His	gaa Glu	ggc Gly 270	ttg Leu	gaa Glu	gaa Glu	934
gat Asp	aaa Lys 275	gac Asp	cat His	cca Pro	aca Thr	act Thr 280	tct Ser	act Thr	ctg Leu	aca Thr	tca Ser 285	agc Ser	aat Asn	agg Arg	aat Asn	982
gat Asp 290	gtc Val	aca Thr	ggg Gly	gga Gly	aga Arg 295	aga Arg	gac Asp	cca Pro	aat Asn	cat His 300	tct Ser	gaa Glu	ggc Gly	tca Ser	act Thr 305	1030

11-88L.ST25.txt

cat tta ctg gaa ggt tat acc tct cat tac cca cac acg aag gaa agc	1078
His Leu Leu Glu Ile Pro Tyr Thr Ser His Tyr Pro His Thr Lys Phe Glu Ser	
agg acc ttc atc cca gtg acc tca gct aag act ggg tcc ttt gga gtt	1126
Arg Thr Phe Val Pro Val Thr Ser Ala Lys Thr Gly Ser Phe Gly Val	
act gca gtt act gtt gga gat tcc aac tct aat gtc aat cgt tcc tta	1174
Thr Ala Val Thr Val Gly Asp Ser Asn Ser Asn Val Asn Arg Ser Leu	
tca gga gac caa gac aca ttc cac ccc agt ggg ggg tcc cat acc act	1222
Ser Gly Asp Gln Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr	
cat gga tct gaa tca gat gga cac tca cat ggg agt caa gaa ggt gga	1270
His Gly Ser Glu Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Gly	
gca aac aca acc tct ggt cct ata agg aca ccc caa att cca gaa tgg	1318
Ala Asn Thr Thr Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp	
ctg atc atc ttg gca tcc ctc ttg gcc ttg gct ttg att ctt gca gtt	1366
Leu Ile Ile Leu Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu Ala Val	
tgc att gca gtc aac agt cga aga agg tgt ggg cag aag aaa aag cta	1414
Cys Ile Ala Val Asn Ser Arg Arg Arg Cys Gly Gln Lys Lys Lys Leu	
gtg atc aac agt ggc aat gga gct gtg gag gac aga aag cca agt gga	1462
Val Ile Asn Ser Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser Gly	
ctc aac gga gag gcc agc aag tct cag gaa atg gtg cat ttg gtg aac	1510
Leu Asn Gly Glu Ala Ser Lys Ser Gln Glu Met Val His Leu Val Asn	
aag gag tcg tca gaa act cca gac cag ttt atg aca gct gat gag aca	1558
Lys Glu Ser Ser Glu Thr Pro Asp Gln Phe Met Thr Ala Asp Glu Thr	
agg aac ctg cag aat gtg gac atg aag att ggg gtg taacacctac	1604
Arg Asn Leu Gln Asn Val Asp Met Lys Ile Gly Val	
accattatct tggaaagaaa caacgttggg aacataacca ttacagggga gctgggacac	1664
ttaacagatg caatgtgcta ctgattgttt catttcgaat ctataatagc ataaattttt	1724
ctactctttt tgttttttgt gttttgttct ttaaagtcag gtccaatttg taaaacagc	1784
attgtcttct gaaattaggg cccaattaat aatcagcaag aattttgatc gtttcagttc	1844
cccacttggg gccctttcat cctcgggtg tgctatggat ggcttctaac aaaaacctac	1904
cacatagtta ttctgtatgc ccaaccttgc cccccaccag ctaaggacat ttccagggtt	1964
aatagggcct ggtcctggga ggaaatttga atgggtcatt ttgcccttcc attagcctaa	2024
tccctgggca ttgctttcca ctgaggttgg gggttgggtt gtactagtta cacatcttca	2084

11-88L.ST25.txt

acagaccccc tctagaaatt tttcagatgc ttctgggaga cacccaaagg gtaagtctat	2144
ttatctgtag taaactattt atctgtgttt ttgaaatatt aaaccttgga tcagtccttt	2204
tattcagtat aattttttaa agttactttg tcagaggcac aaaaagggtt taaactgatt	2264
cataataaat atctgtacct tcttcgaaaa aaaaaaaaaa aaaa	2308

<210> 34
 <211> 493
 <212> PRT
 <213> Homo sapiens

<400> 34

Met Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro	
1 5 10 15	

Leu Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly	
20 25 30	

Val Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu	
35 40 45	

Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala	
50 55 60	

Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly	
65 70 75 80	

Phe Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile	
85 90 95	

Cys Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser	
100 105 110	

Gln Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp	
115 120 125	

Cys Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr	
130 135 140	

Ile Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu	
145 150 155 160	

Tyr Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp	
165 170 175	

Asp Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly	
180 185 190	

11-88L.ST25.txt

Tyr Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp
 195 200 205
 Ser Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Arg Thr Asn Met
 210 215 220
 Asp Ser Ser His Ser Thr Thr Leu Gln Pro Thr Ala Asn Pro Asn Thr
 225 230 235 240
 Gly Leu Val Glu Asp Leu Asp Arg Thr Gly Pro Leu Ser Met Thr Thr
 245 250 255
 Gln Gln Ser Asn Ser Gln Ser Phe Ser Thr Ser His Glu Gly Leu Glu
 260 265 270
 Glu Asp Lys Asp His Pro Thr Thr Ser Thr Leu Thr Ser Ser Asn Arg
 275 280 285
 Asn Asp Val Thr Gly Gly Arg Arg Asp Pro Asn His Ser Glu Gly Ser
 290 295 300
 Thr His Leu Leu Glu Gly Tyr Thr Ser His Tyr Pro His Thr Lys Glu
 305 310 315 320
 Ser Arg Thr Phe Ile Pro Val Thr Ser Ala Lys Thr Gly Ser Phe Gly
 325 330 335
 Val Thr Ala Val Thr Val Gly Asp Ser Asn Ser Asn Val Asn Arg Ser
 340 345 350
 Leu Ser Gly Asp Gln Asp Thr Phe His Pro Ser Gly Gly Ser His Thr
 355 360 365
 Thr His Gly Ser Glu Ser Asp Gly His Ser His Gly Ser Gln Glu Gly
 370 375 380
 Gly Ala Asn Thr Thr Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu
 385 390 395 400
 Trp Leu Ile Ile Leu Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu Ala
 405 410 415
 Val Cys Ile Ala Val Asn Ser Arg Arg Arg Cys Gly Gln Lys Lys Lys
 420 425 430
 Leu Val Ile Asn Ser Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser
 Page 57

435

440

11-88L.ST25.txt
445

Gly Leu Asn Gly Glu Ala Ser Lys Ser Gln Glu Met Val His Leu val
450 455 460

Asn Lys Glu Ser Ser Glu Thr Pro Asp Gln Phe Met Thr Ala Asp Glu
465 470 475 480

Thr Arg Asn Leu Gln Asn Val Asp Met Lys Ile Gly Val
485 490

<210> 35
<211> 1452
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (74)..(730)

<400> 35
ctcaaggata atcactaaat tctgccgaaa ggactgagga acggtgcctg gaaaaggga 60

agaatatcac ggc atg ggc atg agt agc ttg aaa ctg ctg aag tat gtc 109
Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val
1 5 10

ctg ttt ttc ttc aac ttg ctc ttt tgg atc tgt ggc tgc tgc att ttg 157
Leu Phe Phe Phe Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu
15 20 25

ggc ttt ggg atc tac ctg ctg atc cac aac aac ttc gga gtg ctc ttc 205
Gly Phe Gly Ile Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe
30 35 40

cat aac ctc ccc tcc ctc acg ctg ggc aat gtg ttt gtc atc gtg ggc 253
His Asn Leu Pro Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly
45 50 55 60

tct att atc atg gta gtt gcc ttc ctg ggc tgc atg ggc tct atc aag 301
Ser Ile Ile Met Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys
65 70 75

gaa aac aag tgt ctg ctt atg tgc ttc ttc atc ctg ctg ctg att atc 349
Glu Asn Lys Cys Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile
80 85 90

ctc ctt gct gag gtg acc ttg gcc atc ctg ctc ttt gta tat gaa cag 397
Leu Leu Ala Glu Val Thr Leu Ala Ile Leu Leu Phe Val Tyr Glu Gln
95 100 105

aag ctg aat gag tat gtg gct aag ggt ctg acc gac agc atc cac cgt 445
Lys Leu Asn Glu Tyr Val Lys Gly Leu Thr Asp Ser Ile His Arg
110 115 120

tac cac tca gac aat agc acc aag gca gcg tgg gac tcc atc cag tca 493
Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser Ile Gln Ser
125 130 135 140

11-88L.ST25.txt

```

ttt ctg cag tgt tgt ggt ata aat ggc acg agt gat tgg acc agt ggc      541
Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp Thr Ser Gly
               145               150               155

cca cca gca tct tgc ccc tca gat cga aaa gtg gag ggt tgc tat gcg      589
Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly Cys Tyr Ala
               160               165               170

aaa gca aga ctg tgg ttt cat tcc aat ttc ctg tat atc gga atc atc      637
Lys Ala Arg Leu Trp Phe His Ser Asn Phe Leu Tyr Ile Gly Ile Ile
               175               180               185

acc atc tgt gta tgt gtg att gag gtg ttg ggg atg tcc ttt gca ctg      685
Thr Ile Cys Val Cys Val Ile Glu Val Leu Gly Met Ser Phe Ala Leu
               190               195               200

acc ctg aac tgc cag att gac aaa acc agc cag acc ata ggg cta      730
Thr Leu Asn Cys Gln Ile Asp Lys Thr Ser Gln Thr Ile Gly Leu
               205               210               215

tgatctgcag tagttctgtg gtgaagagac ttgtttcatc tccggaaatg caaaaccatt      790

tatagcatga agccctacat gatcactgca ggatgatcct cctcccatcc ttctcccttt      850

taggtccctg tcttatacaa ccagagaagt ggggtgtggc caggcacatc ccatctcagg      910

cagcaagaca atcttttcaat cactgacggc agcagccatg tctctcaaag tggtgaaact      970

aatatctgag catcttttat acaagagagg caaagacaaa ctggatttaa tggcccaaca    1030

tcaaagggtg aacccaggat atgaattttt gcatcttccc attgtcgaat tagtctccag    1090

cctctaaata atgcccagtc ttctcccaa agtcaagcaa gagactagtt gaagggagtt    1150

ctggggccag gctcactgga ccattgtcac aaccctctgt ttctctttga ctaagtgtccc    1210

tggctacagg aattacacag ttctctttct ccaaagggca agatctcatt tcaatttctt    1270

tattagaggg ccttattgat gtgttctaag tctttccaga aaaaaactat ccagtgattt    1330

atatcctgat ttcaaccagt cacttagctg ataatcacag taagaagact tctggtatta    1390

tctctctatc agataagatt ttgttaatgt actattttac tcttcaataa ataaaacagt    1450

tt                                                                    1452

<210> 36
<211> 219
<212> PRT
<213> Homo sapiens

<400> 36
Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val Leu Phe Phe Phe
1 5 10 15

Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile
20 25 30

```

Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro
 35 40 45

Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met
 50 55 60

Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys
 65 70 75 80

Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile Leu Leu Ala Glu
 85 90 95

Val Thr Leu Ala Ile Leu Leu Phe Val Tyr Glu Gln Lys Leu Asn Glu
 100 105 110

Tyr Val Ala Lys Gly Leu Thr Asp Ser Ile His Arg Tyr His Ser Asp
 115 120 125

Asn Ser Thr Lys Ala Ala Trp Asp Ser Ile Gln Ser Phe Leu Gln Cys
 130 135 140

Cys Gly Ile Asn Gly Thr Ser Asp Trp Thr Ser Gly Pro Pro Ala Ser
 145 150 155 160

Cys Pro Ser Asp Arg Lys Val Glu Gly Cys Tyr Ala Lys Ala Arg Leu
 165 170 175

Trp Phe His Ser Asn Phe Leu Tyr Ile Gly Ile Ile Thr Ile Cys Val
 180 185 190

Cys Val Ile Glu Val Leu Gly Met Ser Phe Ala Leu Thr Leu Asn Cys
 195 200 205

Gln Ile Asp Lys Thr Ser Gln Thr Ile Gly Leu
 210 215

<210> 37

<211> 12

<212> DNA

<213> Artificial

<220>

<223> oligonucleotide primer

<400> 37

ctttagagca ca

12

<210> 38

<211> 9

<212> PRT

<213> Artificial

<220>

<223> Synthetic peptide

<220>

<221> VARIANT

<222> (1)..(9)

<223> Xaa at positions 1 and 4 can be any amino acid

<400> 38

Xaa Pro Pro Xaa Ala Ser Ala Leu Pro
1 5

<210> 39

<211> 240

<212> PRT

<213> Homo sapiens

<400> 39

Met Ala Gly Pro Pro Arg Leu Leu Leu Leu Pro Leu Leu Leu Ala Leu
1 5 10 15

Ala Arg Gly Leu Pro Gly Ala Leu Ala Ala Gln Glu Val Gln Gln Ser
20 25 30

Pro His Cys Thr Thr Val Pro Val Gly Ala Ser Val Asn Ile Thr Cys
35 40 45

Ser Thr Ser Gly Gly Leu Arg Gly Ile Tyr Leu Arg Gln Leu Gly Pro
50 55 60

Gln Pro Gln Asp Ile Ile Tyr Tyr Glu Asp Gly Val Val Pro Thr Thr
65 70 75 80

Asp Arg Arg Phe Glu Gly Arg Ile Asp Phe Ser Gly Ser Gln Asp Asn
85 90 95

Leu Thr Ile Thr Met His Arg Leu Gln Leu Ser Asp Thr Gly Thr Tyr
100 105 110

Thr Cys Gln Ala Ile Thr Glu Val Asn Val Tyr Gly Ser Gly Thr Leu
115 120 125

Val Leu Val Thr Glu Glu Gln Ser Gln Gly Trp His Arg Cys Ser Asp
130 135 140

Ala Pro Pro Arg Ala Ser Ala Leu Pro Ala Pro Pro Thr Gly Ser Ala
145 150 155 160

11-88L.ST25.txt

Leu Pro Asp Pro Gln Thr Ala Ser Ala Leu Pro Asp Pro Pro Ala Ala
165 170 175

Ser Ala Leu Pro Ala Ala Leu Ala Val Ile Ser Phe Leu Leu Gly Leu
180 185 190

Gly Leu Gly Val Ala Cys Val Leu Ala Arg Thr Gln Ile Lys Lys Leu
195 200 205

Cys Ser Trp Arg Asp Lys Asn Ser Ala Ala Cys Val Val Tyr Glu Asp
210 215 220

Met Ser His Ser Arg Cys Asn Thr Leu Ser Ser Pro Asn Gln Tyr Gln
225 230 235 240

<210> 40
<211> 311
<212> PRT
<213> Homo sapiens

<400> 40

Met Ser Gln Asn Val Cys Pro Arg Asn Leu Trp Leu Leu Gln Pro Leu
1 5 10 15

Thr Val Leu Leu Leu Leu Ala Ser Ala Asp Ser Gln Ala Ala Ala Pro
20 25 30

Pro Lys Ala Val Leu Lys Leu Glu Pro Pro Trp Ile Asn Val Leu Gln
35 40 45

Glu Asp Ser Val Thr Leu Thr Cys Gln Gly Ala Arg Ser Pro Glu Ser
50 55 60

Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr His Thr
65 70 75 80

Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asp Ser Gly Glu Tyr
85 90 95

Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His Leu Thr
100 105 110

Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu Phe Gln
115 120 125

Glu Gly Glu Thr Ile Met Leu Arg Cys His Ser Trp Lys Asp Lys Pro
130 135 140

11-88L.ST25.txt

Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Gln Lys Phe Ser
145 150 155 160

Arg Leu Asp Pro Thr Phe Ser Ile Pro Gln Ala Asn His Ser His Ser
165 170 175

Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe Ser Ser
180 185 190

Lys Pro Val Thr Ile Thr Val Gln Val Pro Ser Met Gly Ser Ser Ser
195 200 205

Pro Met Gly Ile Ile Val Ala Val Val Ile Ala Thr Ala Val Ala Ala
210 215 220

Ile Val Ala Ala Val Val Ala Leu Ile Tyr Cys Arg Lys Lys Arg Ile
225 230 235 240

Ser Ala Asn Ser Thr Asp Pro Val Lys Ala Ala Gln Phe Glu Pro Pro
245 250 255

Gly Arg Gln Met Ile Ala Ile Arg Lys Arg Gln Leu Glu Glu Thr Asn
260 265 270

Asn Asp Tyr Glu Thr Ala Asp Gly Gly Tyr Met Thr Leu Asn Pro Arg
275 280 285

Ala Pro Thr Asp Asp Asp Lys Asn Ile Tyr Leu Thr Leu Pro Pro Asn
290 295 300

Asp His Val Asn Ser Asn Asn
305 310

<210> 41
<211> 385
<212> PRT
<213> Homo sapiens

<400> 41

Met Gly Cys Arg Arg Thr Arg Glu Gly Pro Ser Lys Ala Met Ile Phe
1 5 10 15

Pro Trp Lys Cys Gln Ser Thr Gln Arg Asp Leu Trp Asn Ile Phe Lys
20 25 30

Leu Trp Gly Trp Thr Met Leu Cys Cys Asp Phe Leu Ala His His Gly
35 40 45

11-88L.ST25.txt

Thr Asp Cys Trp Thr Tyr His Tyr Ser Glu Lys Pro Met Asn Trp Gln
50 55 60

Arg Ala Arg Arg Phe Cys Arg Asp Asn Tyr Thr Asp Leu Val Ala Ile
65 70 75 80

Gln Asn Lys Ala Glu Ile Glu Tyr Leu Glu Lys Thr Leu Pro Phe Ser
85 90 95

Arg Ser Tyr Tyr Trp Ile Gly Ile Arg Lys Ile Gly Gly Ile Trp Thr
100 105 110

Trp Val Gly Thr Asn Lys Ser Leu Thr Glu Glu Ala Glu Asn Trp Gly
115 120 125

Asp Gly Glu Pro Asn Asn Lys Lys Asn Lys Glu Asp Cys Val Glu Ile
130 135 140

Tyr Ile Lys Arg Asn Lys Asp Ala Gly Lys Trp Asn Asp Asp Ala Cys
145 150 155 160

His Lys Leu Lys Ala Ala Leu Cys Tyr Thr Ala Ser Cys Gln Pro Trp
165 170 175

Ser Cys Ser Gly His Gly Glu Cys Val Glu Ile Ile Asn Asn Tyr Thr
180 185 190

Cys Asn Cys Asp Val Gly Tyr Tyr Gly Pro Gln Cys Gln Phe Val Ile
195 200 205

Gln Cys Glu Pro Leu Glu Ala Pro Glu Leu Gly Thr Met Asp Cys Thr
210 215 220

His Ser Leu Gly Asn Phe Ser Phe Ser Ser Gln Cys Ala Phe Ser Cys
225 230 235 240

Ser Glu Gly Thr Asn Leu Thr Gly Ile Glu Glu Thr Thr Cys Gly Pro
245 250 255

Phe Gly Asn Trp Ser Ser Pro Glu Pro Thr Cys Gln Val Ile Gln Cys
260 265 270

Glu Pro Leu Ser Ala Pro Asp Leu Gly Ile Met Asn Cys Ser His Pro
275 280 285

Leu Ala Ser Phe Ser Phe Thr Ser Ala Cys Thr Phe Ile Cys Ser Glu
290 295 300

11-88L.ST25.txt

Gly Thr Glu Leu Ile Gly Lys Lys Lys Thr Ile Cys Glu Ser Ser Gly
 305 310 315 320
 Ile Trp Ser Asn Pro Ser Pro Ile Cys Gln Lys Leu Asp Lys Ser Phe
 325 330 335
 Ser Met Ile Lys Glu Gly Asp Tyr Asn Pro Leu Phe Ile Pro Val Ala
 340 345 350
 Val Met Val Thr Ala Phe Ser Gly Leu Ala Phe Ile Ile Trp Leu Ala
 355 360 365
 Arg Arg Leu Lys Lys Gly Lys Lys Ser Lys Arg Ser Met Asn Asp Pro
 370 375 380
 Tyr
 385